


```

; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-489-448-1704

Alignment Scores:
Pred. No.: 1.88 Length: 103
Score: 54.50 Matches: 8
Percent Similarity: 61.54% Conservative: 0
Best Local Similarity: 61.54% Mismatches: 4
Query Match: 43.25% Indels: 1
DB: 6 Gaps: 1

US-10-775-481A-4 (1-57) x US-10-489-448-1704 (1-103)
QY 16 TGCTCTGAATGTTGTTGTAATCCTGCTTGTAAACGGGTGC 54
DB 45 CysCySSerSerCysCys---ProCysCysArgGlyCys 56

RESULT 7
US-10-938-061-106
; Sequence 106. Application US/10938061
; GENERAL INFORMATION:
; APPLICANT: Cairns, Belinda
; APPLICANT: Chen, Ruihuan
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Koepfen, Hartmut
; APPLICANT: Phillips, Heidi S.
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan D.
; APPLICANT: Smith, Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; APPLICANT: Zakanaka, Chie
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Reed Chae J.
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; TITLE OF INVENTION: Treatment of Tumor
; FILE REFERENCE: P5001R1P8
; CURRENT APPLICATION NUMBER: US/10/938,061
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 10/872,991
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 10/872,972
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 10/241,220
; PRIOR FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US 10/177,488
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 60/299,500
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/301,880
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/323,268
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/557,116
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/598,899
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 106
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-061-106

Alignment Scores:
Pred. No.: 2.22 Length: 690
Score: 54.00 Matches: 7
Percent Similarity: 57.14% Conservative: 1
DB: 5 Mismatches: 5

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; APPLICANT: Olsen, Byron
; TITLE OF INVENTION: A Method for the Production of Transgenic Proteins Useful in the
; FILE REFERENCE: GTC-223 PCT
; CURRENT APPLICATION NUMBER: PCT/US05/05406
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/545,790
; PRIOR FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 1071
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-05406-6

Alignment Scores:
Pred. No.: 2.22 Length: 1071
Score: 54.00 Matches: 7
Percent Similarity: 53.85% Conservative: 0
Best Local Similarity: 53.85% Mismatches: 6
Query Match: 42.86% Indels: 0
DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x PCT-US05-05406-6 (1-1071)

Qy 16 TGCTGTGAATGTGTGTAATCCTGCTTGTAAACGGGTGC 54
Db 261 CysCysGlyAlaCysCysThrCysThrCysGlyGlyCys 273

RESULT 10
US-11-060-291-6
; Sequence 6, Application US/11060291
; GENERAL INFORMATION:
; APPLICANT: Olsen, Byron
; TITLE OF INVENTION: A Method for the Production of Transgenic Proteins Useful in the
; FILE REFERENCE: GTC-223
; CURRENT APPLICATION NUMBER: US/11/060,291
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 60/545,790
; PRIOR FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 1071
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-060-291-6

Alignment Scores:
Pred. No.: 2.22 Length: 1071
Score: 54.00 Matches: 7
Percent Similarity: 53.85% Conservative: 0
Best Local Similarity: 53.85% Mismatches: 6
Query Match: 42.86% Indels: 0
DB: 7 Gaps: 0

US-10-775-481A-4 (1-57) x US-11-060-291-6 (1-1071)

Qy 16 TGCTGTGAATGTGTGTAATCCTGCTTGTAAACGGGTGC 54
Db 261 CysCysGlyAlaCysCysThrCysThrCysGlyGlyCys 273

RESULT 11
US-10-287-436A-285
; Sequence 285, Application US/10287436A
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287.436A
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; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 285
; LENGTH: 1123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-285

Alignment Scores:
Pred. No.: 2.22 Length: 1123
Score: 54.00 Matches: 7
Percent Similarity: 53.85% Conservative: 0
Best Local Similarity: 53.85% Mismatches: 6
Query Match: 42.86% Indels: 0
DB: 6 Gaps: 0

US-10-775-481A-4 (1-57) x US-10-287-436A-285 (1-1123)

Qy 16 TGCTGTGAATGTGTGTAATCCTGCTTGTAAACGGGTGC 54
Db 64 CysCysAlaGlyCysCysThrCysThrCysGlyCys 76

RESULT 12
PCT-US05-03560-6
; Sequence 6, Application PC/TUS0503560
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: ITPKS AS SMODIFIERS OF THE IGFR PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX05-004C-PC
; CURRENT APPLICATION NUMBER: PCT/US05/03560
; CURRENT FILING DATE: 2005-01-27
; PRIOR APPLICATION NUMBER: US60/539,837
; PRIOR FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 3398
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-03560-6

Alignment Scores:
Pred. No.: 2.2 Length: 3398
Score: 54.00 Matches: 7
Percent Similarity: 53.85% Conservative: 0
Best Local Similarity: 53.85% Mismatches: 6
Query Match: 42.86% Indels: 0
DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x PCT-US05-03560-6 (1-3398)

Qy 16 TGCTGTGAATGTGTGTAATCCTGCTTGTAAACGGGTGC 54
Db 2463 CysCysThrCysCysCysThrGlyThrCysAlaGlyCys 2475

RESULT 13
US-60-643-717-5307
; Sequence 5307, Application US/60643717
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)A
; CURRENT APPLICATION NUMBER: US/60/643,717
; CURRENT FILING DATE: 2005-01-12
; NUMBER OF SEQ ID NOS: 19247
; SEQ ID NO 5307
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Kluyveromyces lactis
US-60-643-717-5307
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:39:19 ; Search time 78.4963 Seconds
(without alignments)
282.715 Million cell updates/sec

Title: US-10-775-481A-5

Perfect score: 126

Sequence: 1 NSSNYCELCCNPACNGCY 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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31: /cgn2_6/ptodata/1/paa/US105_COMB.pep.*
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37: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	126	100.0	19	1	PCT-US04-03765-5	Sequence 5, Appli
2	126	100.0	19	1	PCT-US94-12232-5	Sequence 5, Appli
3	126	100.0	19	8	US-08-468-449B-5	Sequence 5, Appli
4	126	100.0	19	16	US-09-263-477-5	Sequence 5, Appli
5	126	100.0	19	16	US-09-263-477A-5	Sequence 5, Appli
6	126	100.0	19	21	US-09-724-983-5	Sequence 5, Appli
7	126	100.0	19	32	US-10-621-684-5	Sequence 5, Appli
8	126	100.0	19	33	US-10-775-481A-5	Sequence 5, Appli
9	120	95.2	19	1	PCT-US02-09551-23	Sequence 23, Appli
10	120	95.2	19	4	US-08-085-126-20	Sequence 20, Appli
11	120	95.2	19	7	US-08-342-241A-31	Sequence 31, Appli
12	120	95.2	19	8	US-08-438-114-20	Sequence 20, Appli
13	120	95.2	19	16	US-09-291-520-31	Sequence 31, Appli
14	120	95.2	19	16	US-09-291-520-31	Sequence 31, Appli
15	120	95.2	19	19	US-09-525-715-2	Sequence 2, Appli
16	120	95.2	19	27	US-10-107-814-23	Sequence 23, Appli
17	120	95.2	19	29	US-10-371-966-1	Sequence 1, Appli
18	120	95.2	19	30	US-10-479-606-7	Sequence 7, Appli
19	120	95.2	19	33	US-10-766-735-1	Sequence 1, Appli
20	120	95.2	19	33	US-10-766-735-26	Sequence 26, Appli
21	120	95.2	19	33	US-10-796-719-1	Sequence 1, Appli
22	120	95.2	19	33	US-10-796-719-26	Sequence 26, Appli
23	120	95.2	21	33	US-10-766-735-39	Sequence 39, Appli
24	120	95.2	21	33	US-10-796-719-39	Sequence 39, Appli
25	120	95.2	72	33	US-10-766-735-21	Sequence 21, Appli
26	120	95.2	72	33	US-10-796-719-21	Sequence 21, Appli
27	118	93.7	19	33	US-10-766-735-84	Sequence 84, Appli
28	118	93.7	19	33	US-10-766-735-86	Sequence 86, Appli
29	118	93.7	19	33	US-10-796-719-84	Sequence 84, Appli
30	118	93.7	19	33	US-10-796-719-86	Sequence 86, Appli
31	117	92.9	19	33	US-10-766-735-92	Sequence 92, Appli
32	117	92.9	19	33	US-10-796-719-92	Sequence 92, Appli
33	116	92.1	19	33	US-10-371-966-2	Sequence 2, Appli
34	116	92.1	19	33	US-10-766-735-27	Sequence 27, Appli
35	116	92.1	19	33	US-10-766-735-87	Sequence 87, Appli
36	116	92.1	19	33	US-10-796-719-27	Sequence 27, Appli
37	116	92.1	19	33	US-10-796-719-87	Sequence 87, Appli
38	116	92.1	21	33	US-10-766-735-40	Sequence 40, Appli
39	116	92.1	21	33	US-10-766-735-41	Sequence 41, Appli
40	116	92.1	21	33	US-10-796-719-40	Sequence 40, Appli
41	116	92.1	21	33	US-10-796-719-41	Sequence 41, Appli
42	115	91.3	19	33	US-10-766-735-28	Sequence 28, Appli
43	115	91.3	19	33	US-10-766-735-75	Sequence 75, Appli
44	115	91.3	19	33	US-10-766-735-79	Sequence 79, Appli
45	115	91.3	19	33	US-10-766-735-90	Sequence 90, Appli

ALIGNMENTS

RESULT 1
PCT-US04-03765-5
; Sequence 5, Application PC/TUS0403765
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; APPLICANT: Pitari, Giovanni Mario
; APPLICANT: Park, Jason
; APPLICANT: Schulz, Stephanie
; APPLICANT: Wolfe, Henry R.
; APPLICANT: Lubbe, Wilhelm
; TITLE OF INVENTION: The Use Of GCC Ligands
; FILE REFERENCE: 08321-168 PCI
; CURRENT APPLICATION NUMBER: PCT/US04/03765
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/446,730
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5

LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ST Ib
PCT-US04-03765-5

Query Match 100.0%; Score 126; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NSSNYCCELCCNPACNGCY 19
Db 1 NSSNYCCELCCNPACNGCY 19

RESULT 2

PCT-US94-12232-5
Sequence 5, Application PC/TUS9412232
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically
Bind To Colorectal Cancer Cells
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Norris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12232
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,056
FILING DATE: 13-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1360
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-12232-5

Query Match 100.0%; Score 126; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCELCCNPACNGCY 19
Db 1 NSSNYCCELCCNPACNGCY 19

RESULT 3

US-08-468-449B-5
Sequence 5, Application US/08468449B
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds And Methods Of Using The Same
FILE REFERENCE: TJU-1588
CURRENT APPLICATION NUMBER: US/08/468,449B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 08/141,892
PRIOR FILING DATE: 1993-10-26
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Novel Sequence
US-08-468-449B-5

Query Match 100.0%; Score 126; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCELCCNPACNGCY 19
Db 1 NSSNYCCELCCNPACNGCY 19

RESULT 4

US-09-263-477-5
Sequence 5, Application US/09263477
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-263-477-5

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Query Match      100.0%; Score 126; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NSSNYCCCLCCNPACNGCY 19
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DB      1 NSSNYCCCLCCNPACNGCY 19
      |||||

RESULT 5
US-09-263-477A-5
; Sequence 5, Application US/09263477A
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,477A
; FILING DATE: 05-Mar-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-263-477A-5

Query Match      100.0%; Score 126; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NSSNYCCCLCCNPACNGCY 19
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DB      1 NSSNYCCCLCCNPACNGCY 19
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RESULT 6
US-09-724-983-5
; Sequence 5, Application US/09724983
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods of Using the Same
; FILE REFERENCE: TJU-2444
; CURRENT APPLICATION NUMBER: US/09/724,983
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 08/468,449

Query Match      100.0%; Score 126; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NSSNYCCCLCCNPACNGCY 19
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DB      1 NSSNYCCCLCCNPACNGCY 19
      |||||

US-09-724-983-5
; Sequence 5, Application US/10621684
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-621-684-5

Query Match      100.0%; Score 126; DB 32; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NSSNYCCCLCCNPACNGCY 19
      |||||
DB      1 NSSNYCCCLCCNPACNGCY 19
      |||||

RESULT 7
US-10-621-684-5
; Sequence 5, Application US/10621684
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-621-684-5

Query Match      100.0%; Score 126; DB 32; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NSSNYCCCLCCNPACNGCY 19
      |||||
DB      1 NSSNYCCCLCCNPACNGCY 19
      |||||

RESULT 8
```

US-10-775-481A-5
; Sequence 5, Application US/10775481A
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; APPLICANT: Pitari, Giovanni Mario
; APPLICANT: Park, Jason
; APPLICANT: Schulz, Stephanie
; APPLICANT: Wolfe, Henry R.
; APPLICANT: Lubbe, Wilhelm
; TITLE OF INVENTION: The Use Of GCC Ligands
; FILE REFERENCE: 08321-0168 US1
; CURRENT APPLICATION NUMBER: US/10/775,481A
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/446,730
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: heat stable toxin peptide Ib
US-10-775-481A-5

Query Match 100.0%; Score 136; DB 33; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
|||||
Db 1 NSSNYCCCLCCNPACNGCY 19

RESULT 9
PCT-US02-09551-23
; Sequence 23, Application PC/TUS0209551
; GENERAL INFORMATION:
; APPLICANT: SYNERGY PHARMACEUTICALS
; TITLE OF INVENTION: GUANYLATE CYCLASE RECEPTOR AGONISTS FOR THE TREATMENT
; FILE REFERENCE: 81361/141030
; CURRENT APPLICATION NUMBER: PCT/US02/09551
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (6)..(10)
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (7)..(15)
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (11)..(18)
PCT-US02-09551-23

Query Match 95.2%; Score 120; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 7.8e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
|||||
Db 1 NSSNYCCCLCCNPACNGCY 19

RESULT 10
US-08-085-126-20
; Sequence 20, Application US/08085126

; GENERAL INFORMATION:
; APPLICANT: LADNER, Robert C.
; APPLICANT: CANNON, Larick E.
; TITLE OF INVENTION: CHELYDRYZYMES AND NEPAZYMES, AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 236
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/085,126
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LADNER=10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-085-126-20
Query Match 95.2%; Score 120; DB 4; Length 19;
Best Local Similarity 94.7%; Pred. No. 7.8e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NSSNYCCCLCCNPACNGCY 19
|||||
Db 1 NSSNYCCCLCCNPACNGCY 19
RESULT 11
US-08-342-241A-31
; Sequence 31, Application US/08342241A
; GENERAL INFORMATION:
; APPLICANT: Holmgren, Jan
; APPLICANT: Lebens, Michael
; TITLE OF INVENTION: IMMUNOGENS FOR STIMULATING MUCOSAL
; TITLE OF INVENTION: IMMUNITY
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,241A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McCormack, Myra H
 ; REGISTRATION NUMBER: 36,602
 ; REFERENCE/DOCKET NUMBER: HOLMG.001A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-235-8550
 ; TELEFAX: 619-235-0176
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 31:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19 amino acids
 ; TYPE: amino acids
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 ; US-08-342-241A-31

Query Match 95.2%; Score 120; DB 7; Length 19;
 Best Local Similarity 94.7%; Pred. No. 7.8e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPACGCGY 19
 Db 1 NSSNYCCCLCCNPACTGCGY 19

RESULT 12

US-08-438-114-20
 ; Sequence 20, Application US/08438114
 ; GENERAL INFORMATION:
 ; APPLICANT: LADNER, Richard C.
 ; APPLICANT: CANNON, Larick E.
 ; TITLE OF INVENTION: CHELYDRYZZYMES AND NEPAZYMES, AND USES
 ; TITLE OF INVENTION: THEREFOR
 ; NUMBER OF SEQUENCES: 240
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/438.114
 ; FILING DATE: 08-MAY-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/308,793
 ; FILING DATE: 19-SEP-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/085,126
 ; FILING DATE: 25-JUN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: COOPER, Iver P.
 ; REGISTRATION NUMBER: 28,005
 ; REFERENCE/DOCKET NUMBER: LADNER=108
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:

; LENGTH: 19 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-438-114-20
 Query Match 95.2%; Score 120; DB 8; Length 19;
 Best Local Similarity 94.7%; Pred. No. 7.8e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPACGCGY 19
 Db 1 NSSNYCCCLCCNPACTGCGY 19

RESULT 13

US-09-291-520-31
 ; Sequence 31, Application US/09291520
 ; GENERAL INFORMATION:
 ; APPLICANT: Holmgren, Jan
 ; APPLICANT: Lebens, Michael
 ; TITLE OF INVENTION: IMMUNOGENS FOR STIMULATING MUCOSAL
 ; TITLE OF INVENTION: IMMUNITY
 ; NUMBER OF SEQUENCES: 51
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobbe, Martens, Olson and Bear
 ; STREET: 620 Newport Center Drive 16th Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/291,520
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/342,241
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McCormack, Myra H
 ; REGISTRATION NUMBER: 36,602
 ; REFERENCE/DOCKET NUMBER: HOLMG.001A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-235-8550
 ; TELEFAX: 619-235-0176
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 31:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19 amino acids
 ; TYPE: amino acids
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 ; US-09-291-520-31

Query Match 95.2%; Score 120; DB 16; Length 19;
 Best Local Similarity 94.7%; Pred. No. 7.8e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPACGCGY 19
 Db 1 NSSNYCCCLCCNPACTGCGY 19

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RESULT 14
US-09-520-31
; Sequence 31, Application US/09291520A
; GENERAL INFORMATION:
; APPLICANT: Holmgren, Jan
; APPLICANT: Lebens, Michael
; TITLE OF INVENTION: IMMUNOGENS FOR STIMULATING MUCOSAL
; TITLE OF INVENTION: IMMUNITY
; FILE REFERENCE: HOLMG.001DVI
; CURRENT APPLICATION NUMBER: US/09/291,520A
; CURRENT FILING DATE: 1999-04-04
; EARLIER APPLICATION NUMBER: 08/342,241
; EARLIER FILING DATE: 1994-11-17
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 19
; TYPE: PRT
; ORGANISM: E. coli
US-09-291-520-31

Query Match          95.2%; Score 120; DB 16; Length 19;
Best Local Similarity 94.7%; Pred. No. 7.8e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
Db 1 NSSNYCCCLCCNPACTGCG 19

RESULT 15
US-09-525-715-2
; Sequence 2, Application US/09525715
; GENERAL INFORMATION:
; APPLICANT: Johnson, David
; APPLICANT: Losco, Patricia
; APPLICANT: Harris, Mary Ann
; APPLICANT: Hagen, Else Kruger
; APPLICANT: Desai, Vinay
; TITLE OF INVENTION: Transplantable Sarcoma
; FILE REFERENCE: Transplantable Sarcoma-NIDN73110
; CURRENT APPLICATION NUMBER: US/09/525,715
; CURRENT FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: 60/124,437
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: GB9907408.0
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-525-715-2

Query Match          95.2%; Score 120; DB 19; Length 19;
Best Local Similarity 94.7%; Pred. No. 7.8e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
Db 1 NSSNYCCCLCCNPACTGCG 19

Search completed: March 26, 2005, 17:10:17
Job time : 79.4963 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:44:35 ; Search time 5.89416 Seconds
(without alignments)
187.395 Million cell updates/sec

Title: US-10-775-481A-5

Perfect score: 126

Sequence: 1 NSSNYCCELCCNPACNGCY 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 260697 seqs, 58133403 residues

Total number of hits satisfying chosen parameters: 260697

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_New.*

- 1: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep.*
- 8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	77.8	18	6	US-10-934-728-24
2	58	46.0	16	7	US-11-066-697-1249
3	56	44.4	282	8	US-60-655-875-128831
4	55	43.7	98	6	US-10-489-448-3215
5	55	43.7	154	6	US-10-489-448-1582
6	54.5	43.3	103	6	US-10-489-448-1704
7	54	42.9	690	6	US-10-938-061-106
8	54	42.9	690	6	US-10-936-626-106
9	54	42.9	1071	1	PCT-US05-05406-6
10	54	42.9	1071	7	US-11-060-291-6
11	54	42.9	1123	6	US-10-287-436A-285
12	54	42.9	3398	1	PCT-US05-03560-6
13	52	41.3	152	8	US-60-655-875-169174
14	52	41.3	158	8	US-60-655-875-163386
15	52	41.3	1435	6	US-10-184-644-581
16	52	41.3	1435	6	US-10-192-007-581
17	51	40.5	111	6	US-10-450-763-55164
18	50.5	40.1	271	8	US-10-450-763-56787
19	50.5	40.1	271	8	US-60-655-875-135230
20	50	39.7	15	6	US-10-934-728-25
21	50	39.7	15	7	US-11-066-697-1247
22	50	39.7	15	7	US-11-066-697-1248
23	50	39.7	309	1	PCT-US04-17965-1363
24	50	39.7	309	1	PCT-US04-17965B-1363
25	50	39.7	358	8	US-60-655-875-132098

26	50	39.7	424	6	US-10-450-763-42525	Sequence 42525, A
27	50	39.7	508	6	US-10-489-448-1646	Sequence 1646, Ap
28	49.5	39.3	206	6	US-10-450-763-59727	Sequence 59727, A
29	49.5	39.3	1200	7	US-11-058-476-3	Sequence 3, Appli
30	49	38.9	12	6	US-10-934-728-22	Sequence 22, Appl
31	49	38.9	162	8	US-60-655-875-165998	Sequence 165998,
32	49	38.9	264	8	US-60-655-875-137235	Sequence 137235,
33	49	38.9	282	8	US-60-655-875-139718	Sequence 139718,
34	49	38.9	857	8	US-60-655-875-153943	Sequence 153943,
35	48.5	38.5	256	6	US-10-450-763-38696	Sequence 38696, A
36	48.5	38.5	351	6	US-10-450-763-54057	Sequence 54057, A
37	48.5	38.5	398	6	US-10-450-763-49367	Sequence 49367, A
38	48.5	38.5	497	6	US-10-287-436A-269	Sequence 269, App
39	48.5	38.5	1501	5	US-09-857-581B-16	Sequence 16, Appl
40	48	38.1	13	7	US-11-066-697-1392	Sequence 1392, Ap
41	48	38.1	156	8	US-60-655-875-162472	Sequence 162472,
42	48	38.1	181	8	US-60-655-875-169804	Sequence 169804,
43	48	38.1	212	8	US-60-655-875-169914	Sequence 169914,
44	48	38.1	221	8	US-60-655-875-162864	Sequence 162864,
45	48	38.1	560	6	US-10-287-436A-220	Sequence 220, App

ALIGNMENTS

RESULT 1
US-10-934-728-24
; Sequence 24, Application US/10934728
; GENERAL INFORMATION:
; APPLICANT: Balloul, Jean Marc
; APPLICANT: Paul, Stephane
; APPLICANT: Geist, Michel
; APPLICANT: Silvestre, Nathalie
; APPLICANT: Erbe, Philippe
; TITLE OF INVENTION: Foxvirus With Targeted Infection Specificity
; FILE REFERENCE: 032751-115
; CURRENT APPLICATION NUMBER: US/10/934,728
; PRIOR FILING DATE: 2004-09-07
; PRIOR APPLICATION NUMBER: US 09/832,899
; PRIOR FILING DATE: 2001-04-14
; PRIOR APPLICATION NUMBER: US 60/246,080
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: EP 0040109.7
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: EP 01440009.7
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sta ligand
US-10-934-728-24
Query Match 77.8%; Score 98; DB 6; Length 18;
Best Local Similarity 93.3%; Pred.No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 YCCELCCNPACNGCY 19
| | | | | | | | | | | | | | | | | | | | | |
Db 4 YCCELCCNPACAGCY 18
RESULT 2
US-11-066-697-1249
; Sequence 1249, Application US/11066697
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Exrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.

Mon Mar 28 09:44:30 2005

us-10-775-481a-5.rapn

APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 50086202301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1249
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-11-066-697-1249

Query Match 46.0%; Score 58; DB 7; Length 16;
Best Local Similarity 75.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 CELCCNPACNGC 18
|||||
Db 4 CELCVNACTGC 15

RESULT 3
US-60-655-875-128831
Sequence 128831, Application US/60655875
GENERAL INFORMATION:
APPLICANT: Boukharov, Andrey
APPLICANT: Du, Zijing
APPLICANT: Guo, Liang
APPLICANT: Kovalic, David
APPLICANT: Lu, Maolong
APPLICANT: McCarter, James
APPLICANT: Miller, Nancy
APPLICANT: Williams, Deryck
APPLICANT: Vaudin, Mark
APPLICANT: Wu, Wei
TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
FILE REFERENCE: 38-21(53885)
CURRENT APPLICATION NUMBER: US/60/655,875
CURRENT FILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
SEQ ID NO 128831
LENGTH: 282
TYPE: PRT
ORGANISM: Heterodera glycines
FEATURE:
OTHER INFORMATION: Coding regions on vcdna: vcdna-SeqID_55254; Strand=-; Position=1-
OTHER INFORMATION: Homolog annotation: Hit ID=XP_311331.1; Match level="QueryCoverag
OTHER INFORMATION: =100%; HitCoverage=100%; E-value=5e-34, Identity=36%; Hit
OTHER INFORMATION: description=ENSANGP00000001657 [Anopheles gambiae]
US-60-655-875-128831

Query Match 44.4%; Score 56; DB 8; Length 282;
Best Local Similarity 52.6%; Pred. No. 3.3;
Matches 10; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 2 SSNVCC--ELCCNPACNGC 18
|||||
Db 239 SSNHCCTSSSCCNHSSNRC 257
|||||

RESULT 4
US-10-489-448-3215
Sequence 3215, Application US/10489448
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Xue, Aidong J.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Wehrman, Tom
APPLICANT: Zhou, Ping
APPLICANT: Ghosh, Malabika
APPLICANT: Wang, Dunrui
APPLICANT: Ma, Yunqing
APPLICANT: Asundi, Vinod
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Gezhi
APPLICANT: Haley-Vicente, Dana
APPLICANT: Dmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 810CIP PCT
CURRENT APPLICATION NUMBER: US/10/489,448
CURRENT FILING DATE: 1004-03-10
PRIOR APPLICATION NUMBER: US 60/324,631
PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/US01/03800
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3476
SOFTWARE: pt_FL_genes Version 6.0
SEQ ID NO 3215
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(98)
OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set fort
US-10-489-448-3215

Query Match 43.7%; Score 55; DB 6; Length 98;
Best Local Similarity 70.0%; Pred. No. 1.7;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCELCNCPAC 15
|||||
Db 16 CCQPCCRPAC 25

RESULT 5
US-10-489-448-1582
Sequence 1582, Application US/10489448
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom


```

; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Ma, Yunqing
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Zhiwei
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: PolyPeptides
; CURRENT APPLICATION NUMBER: US/10/489,448
; CURRENT FILING DATE: 1004-03-10
; PRIOR APPLICATION NUMBER: US 60/324,631
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3476
; SOFTWARE: pc_FL_genes Version 6.0
; SEQ ID NO 1582
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-489-448-1582

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Query Match 43.7%; Score 55; DB 6; Length 154;
Best Local Similarity 70.0%; Pred. No. 2.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy 6 CCELCNCPAC 15
Db 125 CCQPCCRPAC 134

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RESULT 6
US-10-489-448-1704
; Sequence 1704, Application US/10489448
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Ma, Yunqing

```

```

; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: PolyPeptides
; CURRENT APPLICATION NUMBER: US/10/489,448
; CURRENT FILING DATE: 1004-03-10
; PRIOR APPLICATION NUMBER: US 60/324,631
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3476
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 1704
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-489-448-1704

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Query Match 43.3%; Score 54.5; DB 6; Length 103;
Best Local Similarity 61.5%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Qy 6 CCELCNCPACNGC 18
Db 45 CCSSCC-PCCRCG 56

```

```

RESULT 7
US-10-938-061-106
; Sequence 106, Application US/10938061
; GENERAL INFORMATION:
; APPLICANT: Cairns, Belinda
; APPLICANT: Chen, Ruihuan
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Koeppe, Hartmut
; APPLICANT: Phillips, Heidi S.
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan D.
; APPLICANT: Smith, Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; APPLICANT: Sakanaka, Chie
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Reed Chae J.
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; FILE REFERENCE: P5001R1P1B
; CURRENT APPLICATION NUMBER: US/10/938,061
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 10/872,991

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; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 10/872,972
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 10/241,220
; PRIOR FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US 10/177,488
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 60/299,500
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/301,880
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/323,268
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/557,116
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/598,899
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 106
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-061-106

Query Match 42.9%; Score 54; DB 6; Length 690;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 YCCELCNPNACNGC 18
|||:|:|
Db 620 YCCRVCCACCLLC 633

RESULT 8
US-10-936-626-106
; Sequence 106, Application US/10936626
; GENERAL INFORMATION:
; APPLICANT: Cairns, Belinda
; APPLICANT: Chen, Ruihuan
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Koepfen, Hartmut
; APPLICANT: Phillips, Heidi S.
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan D.
; APPLICANT: Smith, Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; TITLE OF INVENTION: Treatment of Tumor
; FILE REFERENCE: P5001R1P1
; CURRENT APPLICATION NUMBER: US/10/936,626
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: US 10/872,991
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 10/872,972
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 10/241,220
; PRIOR FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US 10/177,488
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 60/299,500
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/301,880
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/323,268
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/557,116
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/598,899
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 154

; SEQ ID NO 106
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-936-626-106

Query Match 42.9%; Score 54; DB 6; Length 690;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 YCCELCNPNACNGC 18
|||:|:|
Db 620 YCCRVCCACCLLC 633

RESULT 9
PCT-US05-05406-6
; Sequence 6, Application PC/TUS0505406
; GENERAL INFORMATION:
; APPLICANT: Olsen, Byron
; TITLE OF INVENTION: A Method for the Production of Transgenic Proteins Useful in the
; TITLE OF INVENTION: Treatment of Obesity and Diabetes
; FILE REFERENCE: GTC-223 PCT
; CURRENT APPLICATION NUMBER: PCT/US05/05406
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/545,790
; PRIOR FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 1071
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-05406-6

Query Match 42.9%; Score 54; DB 1; Length 1071;
Best Local Similarity 53.8%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 CCELCNPNACNGC 18
|||:|:|
Db 261 CCGACCTCTCGGC 273

RESULT 10
US-11-060-291-6
; Sequence 6, Application US/11060291
; GENERAL INFORMATION:
; APPLICANT: Olsen, Byron
; TITLE OF INVENTION: A Method for the Production of Transgenic Proteins Useful in the
; TITLE OF INVENTION: Treatment of Obesity and Diabetes
; FILE REFERENCE: GTC-223
; CURRENT APPLICATION NUMBER: US/11/060,291
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 60/545,790
; PRIOR FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 1071
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-060-291-6

Query Match 42.9%; Score 54; DB 7; Length 1071;
Best Local Similarity 53.8%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 CCELCNPNACNGC 18
|||:|:|
Db 261 CCGACCTCTCGGC 273

RESULT 11
US-10-287-436A-285
; Sequence 285, Application US/10287436A
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 285
; LENGTH: 1123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-285

Query Match 42.9%; Score 54; DB 6; Length 1123;
Best Local Similarity 53.8%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 CCELCNPNACNGC 18
Db 64 CCAGCCTTGCTGC 76

RESULT 12
PCT-US05-03560-6
; Sequence 6, Application PC/TUS0503560
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: ITPKS AS SMODIFIERS OF THE IGF1 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX05-004C-PC
; CURRENT APPLICATION NUMBER: PCT/US05/03560
; CURRENT FILING DATE: 2005-01-27
; PRIOR APPLICATION NUMBER: US60/539,837
; PRIOR FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 3398
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-03560-6

Query Match 42.9%; Score 54; DB 1; Length 3398;
Best Local Similarity 53.8%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 CCELCNPNACNGC 18
Db 2463 CCTCCCTGTCAGC 2475

RESULT 13
US-60-655-875-169174
; Sequence 169174, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijing
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Heterodera glycines
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)..(21)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_89809; Strands=-; Position=0-
US-60-655-875-169174

Query Match 41.3%; Score 52; DB 8; Length 158;
Best Local Similarity 53.8%; Pred. No. 6.3;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 NYCCCLCCNPACN 16
Db 41 NICCRCCNCCCS 53

; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 169174
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_95597; Strands=-; Position=3-
US-60-655-875-169174

Query Match 41.3%; Score 52; DB 8; Length 152;
Best Local Similarity 53.8%; Pred. No. 6.1;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 NYCCCLCCNPACN 16
Db 11 NICCRCCNCCCS 23

RESULT 14
US-60-655-875-163386
; Sequence 163386, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijing
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 163386
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Heterodera glycines
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)..(21)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_89809; Strands=-; Position=0-
US-60-655-875-163386

Query Match 41.3%; Score 52; DB 8; Length 158;
Best Local Similarity 53.8%; Pred. No. 6.3;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 NYCCCLCCNPACN 16
Db 41 NICCRCCNCCCS 53

Mon Mar 28 09:44:30 2005

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RESULT 15
US-10-184-644-581
; Sequence 581, Application US/10184644
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 581
; LENGTH: 1435
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-581

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Query Match 41.3%; Score 52; DB 6; Length 1435;
Best Local Similarity 53.8%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 CCELCNPNACNGC 18
Db 1228 CCAACCAGACTAC 1240

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Search completed: March 26, 2005, 17:11:53
Job time : 6.89416 secs

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OM protein - protein search, using sw model
Run on: March 26, 2005, 16:39:19 ; Search time 437.927 Seconds
(without alignments)
282.715 Million cell updates/sec

Title: US-10-775-481A-55
Perfect score: 548
Sequence: 1 MSGQLMAVLLVLSAQ.....LRTIATDELCINVACTGC 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 116806243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
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21: /cgn2_6/ptodata/1/paa/US097_COMB.pep.*
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25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep.*
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28: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
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31: /cgn2_6/ptodata/1/paa/US105_COMB.pep.*
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33: /cgn2_6/ptodata/1/paa/US107_COMB.pep.*
34: /cgn2_6/ptodata/1/paa/US108_COMB.pep.*
35: /cgn2_6/ptodata/1/paa/US109_COMB.pep.*
36: /cgn2_6/ptodata/1/paa/US110_COMB.pep.*
37: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	548	100.0	106	1	PCT-US04-03765-55	Sequence 55, Appl
2	548	100.0	106	33	US-10-775-481A-55	Sequence 55, Appl
3	358	65.3	111	37	US-60-248-592-71	Sequence 71, Appl
4	358	65.3	122	37	US-60-245-228-223	Sequence 223, App
5	356	65.0	112	1	PCT-US04-03765-56	Sequence 56, Appl
6	356	65.0	112	1	PCT-US04-36404-145	Sequence 145, App
7	356	65.0	112	27	US-10-170-205B-19124	Sequence 19124, A
8	356	65.0	112	30	US-10-479-606-5	Sequence 5, Appli
9	356	65.0	112	33	US-10-700-439-145	Sequence 145, App
10	356	65.0	112	33	US-10-775-481A-56	Sequence 56, Appl
11	356	65.0	112	37	US-60-453-050-12227	Sequence 12227, A
12	356	65.0	112	37	US-60-453-135-12227	Sequence 12227, A
13	356	65.0	112	37	US-60-466-412-12227	Sequence 12227, A
14	356	65.0	112	37	US-60-568-073-1020	Sequence 1020, Ap
15	306	55.8	93	23	US-09-834-366-26398	Sequence 26398, A
16	306	55.8	93	37	US-60-197-873-26398	Sequence 26398, A
17	252.5	46.1	109	30	US-10-479-606-6	Sequence 6, Appli
18	166.5	30.4	115	1	PCT-US04-18751-70	Sequence 70, Appl
19	166.5	30.4	115	23	US-09-834-366-17911	Sequence 17911, A
20	166.5	30.4	115	25	US-09-981-353-61	Sequence 61, Appl
21	166.5	30.4	115	26	US-10-003-608-22	Sequence 22, Appl
22	166.5	30.4	115	27	US-10-170-205B-19125	Sequence 19125, A
23	166.5	30.4	115	28	US-10-235-994-22	Sequence 22, Appl
24	166.5	30.4	115	28	US-10-262-473-12	Sequence 12, Appl
25	166.5	30.4	115	30	US-10-479-606-4	Sequence 4, Appli
26	166.5	30.4	115	37	US-60-197-873-17911	Sequence 17911, A
27	166.5	30.4	115	37	US-60-239-841-61	Sequence 61, Appl
28	166.5	30.4	115	37	US-60-453-050-12228	Sequence 12228, A
29	166.5	30.4	115	37	US-60-453-135-12228	Sequence 12228, A
30	166.5	30.4	115	37	US-60-466-412-12228	Sequence 12228, A
31	158	28.8	89	37	US-60-177-670-190	Sequence 190, App
32	122.5	27.8	94	1	PCT-US04-18751-68	Sequence 68, Appl
33	120	21.9	102	1	PCT-US04-18751-71	Sequence 71, Appl
34	120	21.9	102	28	US-10-262-473-14	Sequence 14, Appl
35	120	21.9	108	1	PCT-US04-18751-72	Sequence 72, Appl
36	120	21.9	108	28	US-10-262-473-16	Sequence 16, Appl
37	114	20.8	24	1	PCT-US04-18751-77	Sequence 77, Appl
38	99	18.1	119	22	US-09-791-537-68439	Sequence 68439, A
39	98.5	18.0	23	1	PCT-US04-18751-78	Sequence 78, Appl
40	97.5	17.8	87	1	PCT-US00-05883-1162	Sequence 1162, Ap
41	97.5	17.8	87	24	US-09-925-299-1162	Sequence 1162, Ap
42	90	16.4	15	1	PCT-US04-18751-48	Sequence 48, Appl
43	89	16.2	17	37	US-60-160-203-3643	Sequence 3643, Ap
44	84	15.3	16	1	PCT-US02-09551-20	Sequence 20, Appl
45	84	15.3	16	1	PCT-US04-18751-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1
PCT-US04-03765-55
; Sequence 55, Application PC/TUS0403765
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; APPLICANT: Pitari, Giovanni Mario
; APPLICANT: Park, Jason
; APPLICANT: Schulz, Stephanie
; APPLICANT: Wolfe, Henry R.
; APPLICANT: Lubbe, Wilhelm
; TITLE OF INVENTION: The Use Of GCC Ligands
; FILE REFERENCE: 08321-168 PCI
; CURRENT APPLICATION NUMBER: PCT/US04/03765
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/446,730
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55

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; LENGTH: 106
; TYPE: PRT
; ORGANISM: Rattus norvegicus
PCT-US04-03765-55

Query Match      100.0%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.9e-54;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGSQLMAAVLLLVLSAQGVYIKYHGFQVQLESVKKLNLEEEKOMSDPQQQKSGLLPD 60
Db 1 MSGSQLMAAVLLLVLSAQGVYIKYHGFQVQLESVKKLNLEEEKOMSDPQQQKSGLLPD 60

QY 61 VCYNPALPLDLPVCASQEAASFTFKALRTIATDECELCINVACTGC 106
Db 61 VCYNPALPLDLPVCASQEAASFTFKALRTIATDECELCINVACTGC 106

RESULT 2
US-10-775-481A-55
; Sequence 55, Application US/10775481A
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; APPLICANT: Pitari, Giovanni Mario
; APPLICANT: Park, Jason
; APPLICANT: Schulz, Stephanie
; APPLICANT: Wolfe, Henry R.
; APPLICANT: Lubbe, Wilhelm
; TITLE OF INVENTION: The Use Of GCC Ligands
; FILE REFERENCE: 08321-0168 US1
; CURRENT APPLICATION NUMBER: US/10/775, 481A
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/446,730
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-775-481A-55

Query Match      100.0%; Score 548; DB 33; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.9e-54;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGSQLMAAVLLLVLSAQGVYIKYHGFQVQLESVKKLNLEEEKOMSDPQQQKSGLLPD 60
Db 1 MSGSQLMAAVLLLVLSAQGVYIKYHGFQVQLESVKKLNLEEEKOMSDPQQQKSGLLPD 60

QY 61 VCYNPALPLDLPVCASQEAASFTFKALRTIATDECELCINVACTGC 106
Db 61 VCYNPALPLDLPVCASQEAASFTFKALRTIATDECELCINVACTGC 106

RESULT 3
US-60-248-592-71
; Sequence 71, Application US/60248592
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000961
; CURRENT APPLICATION NUMBER: US/60/248,592
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 111
; TYPE: PRT
; ORGANISM: HUMAN
US-60-248-592-71

Query Match      65.3%; Score 358; DB 37; Length 111;
Best Local Similarity 65.7%; Pred. No. 2.2e-32;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 2 SGSQLMAAVLLLVLSAQGVYIKYHGFQVQLESVKKLNLEEEKOMSDPQQQKSGLLPDV 61
Db 7 SGLLTGVAVLLLVLSAQGVYIQGFRVQLESMMKLSDLAOWAPSPRLQAQSLPAV 66

QY 62 CYNPALPLDLPVCASQEAASFTFKALRTIATDECELCINVACTGC 106
Db 67 CHHPALPDLPVCASQEAASFTFKALRTIATDECELCINVACTGC 111

RESULT 4
US-60-245-228-223
; Sequence 223, Application US/60245228
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000878
; CURRENT APPLICATION NUMBER: US/60/245,228
; CURRENT FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 630
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 122
; TYPE: PRT
; ORGANISM: HUMAN
US-60-245-228-223

Query Match      65.3%; Score 358; DB 37; Length 122;
Best Local Similarity 65.7%; Pred. No. 2.5e-32;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 2 SGSQLMAAVLLLVLSAQGVYIKYHGFQVQLESVKKLNLEEEKOMSDPQQQKSGLLPDV 61
Db 17 SGLLTGVAVLLLVLSAQGVYIQGFRVQLESMMKLSDLAOWAPSPRLQAQSLPAV 76

QY 62 CYNPALPLDLPVCASQEAASFTFKALRTIATDECELCINVACTGC 106
Db 77 CHHPALPDLPVCASQEAASFTFKALRTIATDECELCINVACTGC 121

RESULT 5
PCT-US04-03765-56
; Sequence 56, Application PC/TUS0403765
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; APPLICANT: Pitari, Giovanni Mario
; APPLICANT: Park, Jason
; APPLICANT: Schulz, Stephanie
; APPLICANT: Wolfe, Henry R.
; APPLICANT: Lubbe, Wilhelm
; TITLE OF INVENTION: The Use Of GCC Ligands
; FILE REFERENCE: 08321-168 PC1
; CURRENT APPLICATION NUMBER: PCT/US04/03765
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/446,730
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-03765-56

Query Match      65.0%; Score 356; DB 1; Length 112;
Best Local Similarity 65.7%; Pred. No. 3.8e-32;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;
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QY 2 S G S Q L W A A V L L L L V L Q S A Q G V Y I K Y H G F Q V Q L E S V K K L N E L E E K Q M S D P Q Q O K S G L L P D V 61
D b 7 S G L L P G V A V L L L L L Q S T Q S V Y I Q G F R V Q L E S M K K L S D L E A Q W A P S P R L Q A Q S L L P A V 66

QY 62 C Y N P A L P D L O P V C A S Q E A S T F K A L R T I A T D C E L C I N V A C T G C 106
D b 67 C H P P A L P O D L Q P V C A S Q E A S S I F K T L R T I A N D D C E L C V N V A C T G C 111

RESULT 6
US-10-170-205E-19124
; Sequence 19124, Application US/10170205E
; GENERAL INFORMATION:
; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN CAPTURE AGENTS, AND USES THEREOF
; FILE REFERENCE: CL001381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19124
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-19124

Query Match 65.0%; Score 356; DB 1; Length 112;
Best Local Similarity 65.7%; Pred. No. 3.8e-32;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 2 S G S Q L W A A V L L L L V L Q S A Q G V Y I K Y H G F Q V Q L E S V K K L N E L E E K Q M S D P Q Q O K S G L L P D V 61
D b 7 S G L L P G V A V L L L L L Q S T Q S V Y I Q G F R V Q L E S M K K L S D L E A Q W A P S P R L Q A Q S L L P A V 66

QY 62 C Y N P A L P D L O P V C A S Q E A S T F K A L R T I A T D C E L C I N V A C T G C 106
D b 67 C H P P A L P O D L Q P V C A S Q E A S S I F K T L R T I A N D D C E L C V N V A C T G C 111

RESULT 7
US-10-170-205E-19124
; Sequence 19124, Application US/10170205E
; GENERAL INFORMATION:
; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN CAPTURE AGENTS, AND USES THEREOF
; FILE REFERENCE: CL001381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19124
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-19124

Query Match 65.0%; Score 356; DB 27; Length 112;
Best Local Similarity 65.7%; Pred. No. 3.8e-32;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 2 S G S Q L W A A V L L L L V L Q S A Q G V Y I K Y H G F Q V Q L E S V K K L N E L E E K Q M S D P Q Q O K S G L L P D V 61
D b 7 S G L L P G V A V L L L L L Q S T Q S V Y I Q G F R V Q L E S M K K L S D L E A Q W A P S P R L Q A Q S L L P A V 66

QY 62 C Y N P A L P D L O P V C A S Q E A S T F K A L R T I A T D C E L C I N V A C T G C 106
D b 67 C H P P A L P O D L Q P V C A S Q E A S S I F K T L R T I A N D D C E L C V N V A C T G C 111

RESULT 8
US-10-479-606-5
; Sequence 5, Application US/10479606
; GENERAL INFORMATION:
; APPLICANT: Cetin, Yalcin
; APPLICANT: Savas, Yuksel
; TITLE OF INVENTION: Guanlyate-cyclase C ligand, administered via the airways, for the treatment of respiratory airway problems
; FILE REFERENCE: 03100192aa
; CURRENT APPLICATION NUMBER: US/10/479,606
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: DE10127119.0
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/DE02/02040
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 112
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-479-606-5

Query Match 65.0%; Score 356; DB 30; Length 112;
Best Local Similarity 65.7%; Pred. No. 3.8e-32;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 2 S G S Q L W A A V L L L L V L Q S A Q G V Y I K Y H G F Q V Q L E S V K K L N E L E E K Q M S D P Q Q O K S G L L P D V 61
D b 7 S G L L P G V A V L L L L L Q S T Q S V Y I Q G F R V Q L E S M K K L S D L E A Q W A P S P R L Q A Q S L L P A V 66

QY 62 C Y N P A L P D L O P V C A S Q E A S T F K A L R T I A T D C E L C I N V A C T G C 106
D b 67 C H P P A L P O D L Q P V C A S Q E A S S I F K T L R T I A N D D C E L C V N V A C T G C 111

RESULT 9
US-10-700-439-145
; Sequence 145, Application US/10700439
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: Bayer Healthcare LLC
; APPLICANT: Burgess, Christopher
; APPLICANT: Myerow, Susan
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Molino, Gary
; APPLICANT: Maimonis, Peter
; APPLICANT: Burgart, Lawrence
; APPLICANT: Boardman, Lisa A.
; APPLICANT: Thibodeau, Steven
; APPLICANT: Lewis, Marcia
; TITLE OF INVENTION: Use of Differentially Expressed Nucleic Acid Sequences as Biomarkers for Cancer
; FILE REFERENCE: 1657/2022
; CURRENT APPLICATION NUMBER: US/10/700,439
; CURRENT FILING DATE: 2003-11-04
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-439-145

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Query Match      65.0%; Score 356; DB 33; Length 112;
Best Local Similarity 65.7%; Pred. No. 3.8e-32;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 2 SGSQLWAALLVLLVLSAQAGVYIKYHGFQVQLSVKKNLEBEKQMSDPQQKSGLLPDV 61
DB 7 SGLLPGVAVVLLLLQSTQSVYIQGFRVQLSEMKKLSDLQAQWAPSPRLQAQSLPAV 66

QY 62 CYNPALPLDLPVCASQEAASSTFKALRTIATDECELINACTGC 106
DB 67 CHHPALPQDLQPVCAQEAASSIFKTLRTIANDDCELVCNVACTGC 111

RESULT 10
US-10-775-481A-56
; Sequence 56, Application US/10775481A
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; APPLICANT: Pitari, Giovanni Mario
; APPLICANT: Park, Jason
; APPLICANT: Schulz, Stephanie
; APPLICANT: Wolfe, Henry R.
; APPLICANT: Lubbe, Wilhelm
; TITLE OF INVENTION: The Use Of GCC Ligands
; FILE REFERENCE: 08321-0168 US1
; CURRENT APPLICATION NUMBER: US/10/775,481A
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/446,730
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-481A-56

Query Match      65.0%; Score 356; DB 33; Length 112;
Best Local Similarity 65.7%; Pred. No. 3.8e-32;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 2 SGSQLWAALLVLLVLSAQAGVYIKYHGFQVQLSVKKNLEBEKQMSDPQQKSGLLPDV 61
DB 7 SGLLPGVAVVLLLLQSTQSVYIQGFRVQLSEMKKLSDLQAQWAPSPRLQAQSLPAV 66

QY 62 CYNPALPLDLPVCASQEAASSTFKALRTIATDECELINACTGC 106
DB 67 CHHPALPQDLQPVCAQEAASSIFKTLRTIANDDCELVCNVACTGC 111

RESULT 11
US-60-453-050-12227
; Sequence 12227, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12227
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-12227

Query Match      65.0%; Score 356; DB 37; Length 112;
Best Local Similarity 65.7%; Pred. No. 3.8e-32;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 2 SGSQLWAALLVLLVLSAQAGVYIKYHGFQVQLSVKKNLEBEKQMSDPQQKSGLLPDV 61
DB 7 SGLLPGVAVVLLLLQSTQSVYIQGFRVQLSEMKKLSDLQAQWAPSPRLQAQSLPAV 66

QY 62 CYNPALPLDLPVCASQEAASSTFKALRTIATDECELINACTGC 106
DB 67 CHHPALPQDLQPVCAQEAASSIFKTLRTIANDDCELVCNVACTGC 111

RESULT 12
US-60-453-135-12227
; Sequence 12227, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: TAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12227
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-12227

Query Match      65.0%; Score 356; DB 37; Length 112;
Best Local Similarity 65.7%; Pred. No. 3.8e-32;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 2 SGSQLWAALLVLLVLSAQAGVYIKYHGFQVQLSVKKNLEBEKQMSDPQQKSGLLPDV 61
DB 7 SGLLPGVAVVLLLLQSTQSVYIQGFRVQLSEMKKLSDLQAQWAPSPRLQAQSLPAV 66

QY 62 CYNPALPLDLPVCASQEAASSTFKALRTIATDECELINACTGC 106
DB 67 CHHPALPQDLQPVCAQEAASSIFKTLRTIANDDCELVCNVACTGC 111

RESULT 13
US-60-466-412-12227
; Sequence 12227, Application US/60466412
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: TAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001466
; CURRENT APPLICATION NUMBER: US/60/466,412
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 429241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12227
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-466-412-12227

Query Match      65.0%; Score 356; DB 37; Length 112;
Best Local Similarity 65.7%; Pred. No. 3.8e-32;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 2 SGSQLWAALLVLLVLSAQAGVYIKYHGFQVQLSVKKNLEBEKQMSDPQQKSGLLPDV 61
DB 7 SGLLPGVAVVLLLLQSTQSVYIQGFRVQLSEMKKLSDLQAQWAPSPRLQAQSLPAV 66

QY 62 CYNPALPLDLPVCASQEAASSTFKALRTIATDECELINACTGC 106
DB 67 CHHPALPQDLQPVCAQEAASSIFKTLRTIANDDCELVCNVACTGC 111

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QY 2 SGSQLWAALLVLLVLSAQAGVYIKYHGFQVQLSVKKNLEBEKQMSDPQQKSGLLPDV 61
DB 7 SGLLPGVAVVLLLLQSTQSVYIQGFRVQLSEMKKLSDLQAQWAPSPRLQAQSLPAV 66

QY 62 CYNPALPLDLPVCASQEAASSTFKALRTIATDECELINACTGC 106
DB 67 CHHPALPQDLQPVCAQEAASSIFKTLRTIANDDCELVCNVACTGC 111

RESULT 12
US-60-453-135-12227
; Sequence 12227, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: TAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12227
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-12227

Query Match      65.0%; Score 356; DB 37; Length 112;
Best Local Similarity 65.7%; Pred. No. 3.8e-32;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 2 SGSQLWAALLVLLVLSAQAGVYIKYHGFQVQLSVKKNLEBEKQMSDPQQKSGLLPDV 61
DB 7 SGLLPGVAVVLLLLQSTQSVYIQGFRVQLSEMKKLSDLQAQWAPSPRLQAQSLPAV 66

QY 62 CYNPALPLDLPVCASQEAASSTFKALRTIATDECELINACTGC 106
DB 67 CHHPALPQDLQPVCAQEAASSIFKTLRTIANDDCELVCNVACTGC 111

RESULT 13
US-60-466-412-12227
; Sequence 12227, Application US/60466412
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: TAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001466
; CURRENT APPLICATION NUMBER: US/60/466,412
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 429241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12227
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-466-412-12227

Query Match      65.0%; Score 356; DB 37; Length 112;
Best Local Similarity 65.7%; Pred. No. 3.8e-32;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 2 SGSQLWAALLVLLVLSAQAGVYIKYHGFQVQLSVKKNLEBEKQMSDPQQKSGLLPDV 61
DB 7 SGLLPGVAVVLLLLQSTQSVYIQGFRVQLSEMKKLSDLQAQWAPSPRLQAQSLPAV 66

QY 62 CYNPALPLDLPVCASQEAASSTFKALRTIATDECELINACTGC 106
DB 67 CHHPALPQDLQPVCAQEAASSIFKTLRTIANDDCELVCNVACTGC 111

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RESULT 14
US-60-568-073-1020
; Sequence 1020, Application US/60568073
; GENERAL INFORMATION:
; APPLICANT: Huang, Fei
; APPLICANT: Han, Xia
; APPLICANT: Shaw, Peter
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: COLON CANCER BIOMARKERS
; FILE REFERENCE: 10205 PSP
; CURRENT APPLICATION NUMBER: US/60/568,073
; CURRENT FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 1305
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1020
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-568-073-1020
Query Match 65.0%; Score 356; DB 37; Length 112;
Best Local Similarity 65.7%; Pred. No. 3.8e-32;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

Qy 2 SCSQLWAIVLLLLVLSQAGVYIKTHGFQVQLSVKLNLEEEKQMSDPQOQKSGLLPDV 61
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
7 SGLLPGVAVVLLLLQSTQSVYIQGFRVQLSKKLSLEAQWAPSPRLQAQSLPAV 66
Qy 62 CYNPALPLDLQPVCAQAASTFKALRTIATDECELCINVACTGC 106
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
67 CHHPALPDQLQPVCAQAASTFKALRTIATDECELCINVACTGC 111

RESULT 15
US-09-834-366-26398
; Sequence 26398, Application US/09834366
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81.US2.REG
; CURRENT APPLICATION NUMBER: US/09/834,366
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/197,873
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 26398
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-366-26398
Query Match 55.8%; Score 306; DB 23; Length 93;
Best Local Similarity 67.5%; Pred. No. 1.7e-26;
Matches 56; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

Qy 24 IKYHGFQVQLSVKLNLEEEKQMSDPQOQKSGLLPDVCYNPALPLDLQPVCAQAAST 83
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
10 LKYQGFRVQLSKKLSLEAQWAPSPRLQAQSLPAVCHHPALPDQLQPVCAQAAST 69
Qy 84 FKALRTIATDECELCINVACTGC 106
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
70 FKLRTIATDECELCINVACTGC 92
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Search completed: March 26, 2005, 17:10:17
Job time : 437.927 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:44:35 ; Search time 32.8832 Seconds
(without alignments)
187.395 Million cell updates/sec

Title: US-10-775-481A-55
Perfect score: 548
Sequence: 1 MSGQLWAIVLLLVLSQAQ.....LRTIATDCELCINVACTGC 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 260697 seqs, 58133403 residues

Total number of hits satisfying chosen parameters: 260697

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_New.*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep.*
8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	14.8	16	7	US-11-066-697-1249
2	73	13.3	1139	1	PCT-US05-03483-6
3	69.5	12.7	1959	1	PCT-US04-42360-1382
4	69.5	12.7	1959	1	PCT-US04-42360-1384
5	68	12.4	201	8	US-60-655-875-169824
6	68	12.4	295	8	US-60-655-875-162848
7	66.5	12.1	212	8	US-10-450-763-34297
8	65.5	12.0	218	8	US-60-655-875-161554
9	65.5	12.0	218	8	US-60-655-875-161177
10	65.5	12.0	271	8	US-60-655-875-162900
11	65.5	12.0	516	6	US-10-483-448-1225
12	65	11.9	341	6	US-10-450-763-36316
13	64.5	11.8	1225	6	US-10-450-763-41984
14	64.5	11.8	1307	6	US-10-450-763-41544
15	64	11.7	331	8	US-60-643-717-2766
16	64	11.7	700	7	US-11-031-175-14225
17	63	11.5	304	6	US-10-450-763-37880
18	63	11.5	539	6	US-10-450-763-36871
19	63	11.5	539	6	US-10-450-763-56899
20	63	11.5	840	1	PCT-US04-32678-1
21	63	11.5	840	6	US-10-679-102-1
22	63	11.5	840	6	US-10-436-715A-39
23	63	11.5	840	6	US-10-436-715A-69
24	62.5	11.4	166	8	US-60-655-875-165482
25	62.5	11.4	321	6	US-10-450-763-57226

26	62.5	11.4	631	8	US-60-643-717-9245	Sequence 9245, Ap
27	62.5	11.4	646	7	US-11-031-175-12044	Sequence 12044, A
28	62	11.3	280	8	US-60-655-875-162823	Sequence 162823, A
29	62	11.3	280	8	US-60-655-875-168716	Sequence 168716, A
30	62	11.3	330	7	US-11-031-175-10987	Sequence 10987, A
31	62	11.3	436	1	PCT-US04-17965-1428	Sequence 1428, Ap
32	62	11.3	436	1	PCT-US04-17965B-1428	Sequence 1428, Ap
33	62	11.3	472	6	US-10-450-763-44468	Sequence 44468, A
34	62	11.3	982	6	US-10-450-763-53050	Sequence 53050, A
35	62	11.3	1332	1	PCT-US05-01469-4	Sequence 4, Appl
36	62	11.3	1344	6	US-10-450-763-53052	Sequence 53052, A
37	62	11.3	1359	1	PCT-US05-01469-44	Sequence 44, Appl
38	61.5	11.2	257	8	US-60-655-875-150648	Sequence 150648, A
39	61.5	11.2	472	7	US-11-021-951-136	Sequence 136, App
40	61.5	11.2	1331	1	PCT-US05-01469-2	Sequence 2, Appl
41	61	11.1	65	6	US-10-450-763-40066	Sequence 40066, A
42	61	11.1	65	6	US-10-450-763-54287	Sequence 54287, A
43	61	11.1	138	6	US-10-450-763-31187	Sequence 31187, A
44	61	11.1	199	6	US-10-450-763-56918	Sequence 56918, A
45	61	11.1	352	6	US-10-450-763-31174	Sequence 31174, A

ALIGNMENTS

RESULT 1
US-11-066-697-1249
; Sequence 1249, Application US/11066697
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1249
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1249

Query Match 14.8%; Score 81; DB 7; Length 16;
Best Local Similarity 85.7%; Pred. No. 0.0043;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 93 DECELCINVACTGC 106
|:||||:|||||
Db 2 DDCELCNVACTGC 15

RESULT 2
PCT-US05-03483-6
; Sequence 6, Application PC/TUS0503483
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: MAN2AS AS MODIFIERS OF THE IGFR PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX05-005


```

; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 162848
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Homolog annotation: Hit ID=NP_506153.1; Match level="QueryCoverage
; OTHER INFORMATION: =99%, HitCoverage=15%, E-value=3e-53, Identity=38%", Hit descrip
; OTHER INFORMATION: =TMO (5N87) [Caenorhabditis elegans] emb|CAA98425.1| Hypothesica
; OTHER INFORMATION: protein C14C10.5 [Caenorhabditis elegans
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_89271; Strand=+; Position=2-
US-60-655-875-162848

Query Match 12.4%; Score 68; DB 8; Length 295;
Best Local Similarity 23.7%; Pred. No. 5.1;
Matches 27; Conservative 17; Mismatches 38; Indels 32; Gaps 4;

Qy 5 QLVAAVLLLVLSAQG-----VYIKYHGFQVLESVKKLNLELEKQMSDPQQQ 53
Db 45 QLVAAVLLLVLSAQG-----VYIKYHGFQVLESVKKLNLELEKQMSDPQQQ 53

Qy 54 KSGLLPDVCYNPALPL-DLPVCASQEAATF-----KALRTIATDE 94
Db 101 ----YPGICHKPAWLPDKQKLGFEAREICGNRENFLALAEKLLTIKDE 150

RESULT 7
US-10-450-763-34297
; Sequence 34297, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR FILING DATE: 2003-06-11
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 34297
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-34297

Query Match 12.1%; Score 66.5; DB 6; Length 218;
Best Local Similarity 32.6%; Pred. No. 5.2;
Matches 30; Conservative 15; Mismatches 32; Indels 15; Gaps 5;

Qy 1 MSGQLNAVLLLVLSAQGVYIKYHGFQVLESVKKLNLELEKQMSDPQQQKSGLLPD 60
Db 107 MERMQLWAMRLDLRLDQ-----RHLRFGV-LAAGFNLPPEEEEEERKGLLP 158
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Qy 61 VCYNPALPLDLQ-PVCAS-QEAATFFKALRTI 90
Db 159 -----ALGSALQGAQVSWPQLLSTYRLHSL 185

RESULT 8
US-60-655-875-161554
; Sequence 161554, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 161554
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Homolog annotation: Hit ID=CAE60769.1; Match level="QueryCoverage
; OTHER INFORMATION: =100%, HitCoverage=66%, E-value=6e-80, Identity=64%", Hit descrip
; OTHER INFORMATION: Hypothesical protein CBG04457 [Caenorhabditis briggsae]
; FEATURE:
; OTHER INFORMATION: Gene Ontology: Mol. function=protein binding; Cellular component
; OTHER INFORMATION: =cytoplasm; Biological process=protein folding
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_87977; Strand=+; Position=3-
US-60-655-875-161554

Query Match 12.0%; Score 65.5; DB 8; Length 212;
Best Local Similarity 27.2%; Pred. No. 6.6;
Matches 22; Conservative 10; Mismatches 34; Indels 15; Gaps 3;

Qy 34 ESVKKLNLELEKQMSDP-----QQQKSGLLPDVC--YNPALPLDLQPVCSQEA 80
Db 78 ELAKEVMEQKAYIDPELSDEKKNLGNQLFKKGDYFGAMRHYNELKRNPDNAVLYSNR 137

Qy 81 ASTFKALRTI--ATDECELCI 99
Db 138 AACFTKLMEFQRAVDDCDLCL 158

RESULT 9
US-60-655-875-161177
; Sequence 161177, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
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; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 161177
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Homolog annotation: Hit ID=CAB60769.1; Match level="QueryCoverage
; OTHER INFORMATION: =100%, HitCoverage=68%, E-value=5e-83, Identity=64%"; Hit descrip
; OTHER INFORMATION: Hypothetical protein CBG04457 [Caenorhabditis briggsae]
; FEATURE:
; OTHER INFORMATION: Gene Ontology: Mol. function=protein binding; Cellular component
; OTHER INFORMATION: =cytoplasm; Biological process=protein folding
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_87600; Strand=+; Position=1-
US-60-655-875-161177

Query Match      12.0%; Score 65.5; DB 8; Length 218;
Best Local Similarity 27.2%; Pred. No. 6.8;
Matches 22; Conservative 10; Mismatches 34; Indels 15; Gaps 3;

QY 34 ESVKKLNLEEKQMSDP-----QQQKSGLLPDVC--YNPALPLDLQPVCAQEA 80
DB 83 ELAKEVKEMEQKAYIDPELSDKEKNLGNQLFKKGYDPCGAMRHYNEAIKRNPNNAVLYSNR 142
QY 81 ASTFKALRTI--ATDECELICI 99
DB 143 AACFTKLMFQRAVDDCDLCL 163

RESULT 10
US-60-655-875-162900
; Sequence 162900, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijing
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; FILE REFERENCE: IN PLANTS AND COMPOSITIONS THEREOF
; CURRENT APPLICATION NUMBER: US/60/655,875
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 162900
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Hit ID=CAB60769.1; Match level="QueryCoverage
; OTHER INFORMATION: =99%, HitCoverage=84%, E-value=1e-101, Identity=62%"; Hit descrip
; OTHER INFORMATION: Hypothetical protein CBG04457 [Caenorhabditis briggsae]
; FEATURE:
; OTHER INFORMATION: Gene Ontology: Mol. function=UDP-N-acetylglucosamine-peptide N
; OTHER INFORMATION: =acetylglucosaminyltransferase activity; Cellular component
; OTHER INFORMATION: =perinuclear space; Biological process=protein folding
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_89323; Strand=+; Position=84
US-60-655-875-162900

Query Match      12.0%; Score 65.5; DB 8; Length 271;
Best Local Similarity 27.2%; Pred. No. 9;
Matches 22; Conservative 10; Mismatches 34; Indels 15; Gaps 3;

QY 34 ESVKKLNLEEKQMSDP-----QQQKSGLLPDVC--YNPALPLDLQPVCAQEA 80
DB 122 ELAKEVKEMEQKAYIDPELSDKEKNLGNQLFKKGYDPCGAMRHYNEAIKRNPNNAVLYSNR 181
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QY 81 ASTFKALRTI--ATDECELICI 99
DB 182 AACFTKLMFQRAVDDCDLCL 202

RESULT 11
US-10-489-448-1225
; Sequence 1225, Application US/10489448
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Ma, Yungqing
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 810CIP PCT
; CURRENT APPLICATION NUMBER: US/10/489,448
; CURRENT FILING DATE: 1004-03-10
; PRIOR APPLICATION NUMBER: US 60/324,631
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3476
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 1225
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-489-448-1225

Query Match      12.0%; Score 65.5; DB 6; Length 516;
Best Local Similarity 31.6%; Pred. No. 20;
Matches 25; Conservative 15; Mismatches 26; Indels 13; Gaps 4;

QY 10 VLLLVLSAQG-----VYKYHGFQVQLSVKLNLELEKQMSDPQQKSGLLPDVC 62
DB 71 LLELVLSQFLSILPEEFQIWIYQHNPSGEEAVTLLEDL-ERFDDPQQQ-----VPASP 125
QY 63 YNPALP-LDLOQPVCAQEA 80
DB 126 QGPVFPWKDLTCLRASQES 144

RESULT 12
```

```
US-10-450-763-36316
; Sequence 36316, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 36316
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (91)..(204)
; OTHER INFORMATION: ZAP domain identified by Pfam, accession name ZAP, E-value=
; OTHER INFORMATION: 6.3e-19, Pfam score of 76.3
US-10-450-763-36316

Query Match      11.9%; Score 65; DB 6; Length 341;
Best Local Similarity 22.7%; Pred. No. 14;
Matches 17; Conservative 21; Mismatches 21; Indels 16; Gaps 3;

Qy 23 YIKYHGFQVLESVKKLENE-----LEKQMSDPQOKSGLLPDVVCYNPALPDLQPVCA 76
Db 156 YVDYKQYQYDI-TVSDLNQPMVLVSLKKKRNDSQAHLIPELCFPTGL----- 205
Qy 77 SQEAASTFKALRTIA 91
Db 206 TDQATSDPQLMKAVA 220

RESULT 13
US-10-450-763-41984
; Sequence 41984, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 41984
; LENGTH: 1225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (863)..(908)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354N, p-value=1.000e-40, raw score
; OTHER INFORMATION: 13.17
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1225)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-41984
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Query Match      11.8%; Score 64.5; DB 6; Length 1225;
Best Local Similarity 22.8%; Pred. No. 76;
Matches 26; Conservative 18; Mismatches 37; Indels 33; Gaps 4;

Qy 2 SGSOLMAA-----VLLLLVLQSAQGYVIKYHGFQVLESVKKLELEEKQMSDPQOK 54
Db 373 SGSNICCAPISAVLQLLLLIPRTGSGVDLQQTPTDLQLR-VLVNVRRTNKKQKQHPHQ-- 429
Qy 55 SGLLPDVCYNPALPDLQPVCAEQEAASATFKA-----LRTIATDECELCINVA 102
Db 430 -----NPICMSPSSKTKESLKDLMELKTKARELCECTSL 466

RESULT 14
US-10-450-763-41544
; Sequence 41544, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 41544
; LENGTH: 1307
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (896)..(941)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354N, p-value=1.000e-40, raw score
; OTHER INFORMATION: 13.17
US-10-450-763-41544

Query Match      11.8%; Score 64.5; DB 6; Length 1307;
Best Local Similarity 22.8%; Pred. No. 83;
Matches 26; Conservative 18; Mismatches 37; Indels 33; Gaps 4;

Qy 2 SGSOLMAA-----VLLLLVLQSAQGYVIKYHGFQVLESVKKLELEEKQMSDPQOK 54
Db 406 SGSNICCAPISAVLQLLLLIPRTGSGVDLQQTPTDLQLR-VLVNVRRTNKKQKQHPHQ-- 462
Qy 55 SGLLPDVCYNPALPDLQPVCAEQEAASATFKA-----LRTIATDECELCINVA 102
Db 463 -----NPICMSPSSKTKESLKDLMELKTKARELCECTSL 499

RESULT 15
US-60-643-717-2766
; Sequence 2766, Application US/60643717
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)A
; CURRENT APPLICATION NUMBER: US/60/643,717
; CURRENT FILING DATE: 2005-01-12
; NUMBER OF SEQ ID NOS: 19247
; SEQ ID NO 2766
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Crocosphaera watsonii WH 8501
US-60-643-717-2766

Query Match      11.7%; Score 64; DB 8; Length 331;
Best Local Similarity 25.0%; Pred. No. 17;
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	Matches	21;	Conservative	14;	Mismatches	35;	Indels	14;	Gaps	4;
Qy	17	QSAAGVYIKYHGFQVQLESVKLNELEEKQMSDPQOQKSGLLPDCVNCYNPALPLDLQPVCA	76							
Db	146	QKQGVY-----DASIRAIKLNQLGYGH--DP-----NLVLDLVYNPPPSN-KKFSL	191							
Qy	77	SOEAASTFKALRTIATDECELCIN	100							
Db	192	TPEQIKLEKDYKNFLKDNFNCFN	215							

Search completed: March 26, 2005, 17:11:53
 Job time : 32.8832 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: March 26, 2005, 16:39:19 ; Search time 462.715 Seconds
(without alignments)
282.715 Million cell updates/sec

Title: US-10-775-481A-56
Perfect score: 579
Sequence: 1 MGRASGLPGVAVLLLL.....RTIANDCELGVNACTGCL 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_Main:
1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US080_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/1/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/1/paa/US090_COMB.pep.*
15: /cgn2_6/ptodata/1/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/1/paa/US092_COMB.pep.*
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18: /cgn2_6/ptodata/1/paa/US094_COMB.pep.*
19: /cgn2_6/ptodata/1/paa/US095_COMB.pep.*
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21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep.*
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26: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
28: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
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30: /cgn2_6/ptodata/1/paa/US104_COMB.pep.*
31: /cgn2_6/ptodata/1/paa/US105_COMB.pep.*
32: /cgn2_6/ptodata/1/paa/US106_COMB.pep.*
33: /cgn2_6/ptodata/1/paa/US107_COMB.pep.*
34: /cgn2_6/ptodata/1/paa/US108_COMB.pep.*
35: /cgn2_6/ptodata/1/paa/US109_COMB.pep.*
36: /cgn2_6/ptodata/1/paa/US110_COMB.pep.*
37: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	100.0	112	1	PCT-US04-03765-56 Sequence 56, Appl
2	579	100.0	112	1	PCT-US04-36404-145 Sequence 145, App
3	579	100.0	112	27	US-10-170-205B-19124 Sequence 19124, A
4	579	100.0	112	30	US-10-479-606-5 Sequence 5, Appli
5	579	100.0	112	33	US-10-700-439-145 Sequence 145, App
6	579	100.0	112	33	US-10-775-481A-56 Sequence 56, Appl
7	579	100.0	112	37	US-60-453-050-12227 Sequence 12227, A
8	579	100.0	112	37	US-60-453-135-12227 Sequence 12227, A
9	579	100.0	112	37	US-60-466-412-12227 Sequence 12227, A
10	579	100.0	112	37	US-60-568-073-1020 Sequence 1020, Ap
11	571	98.6	122	37	US-60-245-228-223 Sequence 223, App
12	567	97.9	111	37	US-60-248-592-71 Sequence 71, Appl
13	440	76.0	93	23	US-09-834-366-26398 Sequence 26398, A
14	440	76.0	93	37	US-60-197-873-26398 Sequence 26398, A
15	356	61.5	106	1	PCT-US04-03765-55 Sequence 55, Appl
16	356	61.5	106	33	US-10-775-481A-55 Sequence 55, Appl
17	271.5	46.9	89	37	US-60-177-670-190 Sequence 190, App
18	252	43.5	109	30	US-10-479-606-6 Sequence 6, Appli
19	216	37.3	85	1	PCT-US00-05883-1527 Sequence 1527, Ap
20	216	37.3	85	24	US-09-925-299-1527 Sequence 1527, Ap
21	162.5	28.1	94	1	PCT-US04-18751-68 Sequence 68, Appl
22	162.5	28.1	115	23	US-09-834-366-17911 Sequence 70, Appl
23	162.5	28.1	115	23	US-09-834-366-17911 Sequence 70, Appl
24	162.5	28.1	115	25	US-09-981-353-61 Sequence 61, Appl
25	162.5	28.1	115	26	US-10-003-608-22 Sequence 22, Appl
26	162.5	28.1	115	27	US-10-170-205B-19125 Sequence 22, Appl
27	162.5	28.1	115	28	US-10-235-994-22 Sequence 22, Appl
28	162.5	28.1	115	28	US-10-262-473-12 Sequence 12, Appl
29	162.5	28.1	115	30	US-10-479-606-4 Sequence 4, Appli
30	162.5	28.1	115	37	US-60-197-873-17911 Sequence 17911, A
31	162.5	28.1	115	37	US-60-239-841-61 Sequence 61, Appl
32	162.5	28.1	115	37	US-60-453-050-12228 Sequence 12228, A
33	162.5	28.1	115	37	US-60-453-135-12228 Sequence 12228, A
34	162.5	28.1	115	37	US-60-466-412-12228 Sequence 12228, A
35	136	23.5	108	1	PCT-US04-18751-72 Sequence 72, Appl
36	136	23.5	108	28	US-10-262-473-16 Sequence 16, Appl
37	135	23.3	30	37	US-60-187-385-887 Sequence 887, App
38	135	23.3	30	37	US-60-234-446-896 Sequence 896, App
39	134	23.1	24	1	PCT-US04-18751-77 Sequence 77, Appl
40	132	22.8	102	1	PCT-US04-18751-71 Sequence 71, Appl
41	132	22.8	102	28	US-10-262-473-14 Sequence 14, Appl
42	118.5	20.5	23	1	PCT-US04-18751-78 Sequence 78, Appl
43	106	18.3	24	37	US-60-160-203-4187 Sequence 4187, Ap
44	106	18.3	24	37	US-60-169-840-6139 Sequence 6139, Ap
45	100	17.3	17	37	US-60-160-203-3643 Sequence 3643, Ap

ALIGNMENTS

RESULT 1
PCT-US04-03765-56
; Sequence 56, Application PC/TUS0403765
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; APPLICANT: Pitari, Giovanni Mario
; APPLICANT: Park, Jason
; APPLICANT: Schulz, Stephanie
; APPLICANT: Wolfe, Henry R.
; APPLICANT: Lubbe, Wilhelm
; TITLE OF INVENTION: The Use Of GCC Ligands
; FILE REFERENCE: 08321-168 PC1
; CURRENT APPLICATION NUMBER: PCT/US04/03765
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/446,730
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56

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; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-03765-56

Query Match      100.0%; Score 579; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGCRAASGLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLQAQWAPSPRLQAQ 60
    |||||
Db 1 MGCRAASGLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLQAQWAPSPRLQAQ 60
    |||||
QY 61 SLTPAVCHHPALPQDLQPVCSQEQASSIFKTLRTIANDDCELCVNVACTGCL 112
    |||||
Db 61 SLTPAVCHHPALPQDLQPVCSQEQASSIFKTLRTIANDDCELCVNVACTGCL 112
    |||||

RESULT 2
PCT-US04-36404-145
; Sequence 145, Application PC/TUS0436404
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: Bayer Healthcare LLC
; APPLICANT: Burgess, Christopher
; APPLICANT: Myerow, Susan
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Maimonis, Peter
; APPLICANT: Molino, Gary
; APPLICANT: Burtgart, Lawrence
; APPLICANT: Boardman, Lisa A.
; APPLICANT: Thibodeau, Steven
; APPLICANT: Lewis, Marcia
; TITLE OF INVENTION: Use of Differentially Expressed Nucleic Acid Sequences as
; FILE REFERENCE: 1657/2022
; CURRENT APPLICATION NUMBER: PCT/US04/36404
; CURRENT FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-36404-145

Query Match      100.0%; Score 579; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGCRAASGLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLQAQWAPSPRLQAQ 60
    |||||
Db 1 MGCRAASGLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLQAQWAPSPRLQAQ 60
    |||||
QY 61 SLTPAVCHHPALPQDLQPVCSQEQASSIFKTLRTIANDDCELCVNVACTGCL 112
    |||||
Db 61 SLTPAVCHHPALPQDLQPVCSQEQASSIFKTLRTIANDDCELCVNVACTGCL 112
    |||||

RESULT 3
US-10-170-205E-19124
; Sequence 19124, Application US/10170205E
; GENERAL INFORMATION:
; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; FILE REFERENCE: CL001381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19124
; LENGTH: 112
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-19124

Query Match      100.0%; Score 579; DB 27; Length 112;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGCRAASGLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLQAQWAPSPRLQAQ 60
    |||||
Db 1 MGCRAASGLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLQAQWAPSPRLQAQ 60
    |||||
QY 61 SLTPAVCHHPALPQDLQPVCSQEQASSIFKTLRTIANDDCELCVNVACTGCL 112
    |||||
Db 61 SLTPAVCHHPALPQDLQPVCSQEQASSIFKTLRTIANDDCELCVNVACTGCL 112
    |||||

RESULT 4
US-10-479-606-5
; Sequence 5, Application US/10479606
; GENERAL INFORMATION:
; APPLICANT: Cetin, Yalcin
; APPLICANT: Savas, Yusef
; TITLE OF INVENTION: Guanylate-cyclase C ligand, administered via the airways, for the
; FILE REFERENCE: 03100192aa
; CURRENT APPLICATION NUMBER: US/10/479,606
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: DE10127119.0
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/DE02/02040
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-479-606-5

Query Match      100.0%; Score 579; DB 30; Length 112;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGCRAASGLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLQAQWAPSPRLQAQ 60
    |||||
Db 1 MGCRAASGLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLQAQWAPSPRLQAQ 60
    |||||
QY 61 SLTPAVCHHPALPQDLQPVCSQEQASSIFKTLRTIANDDCELCVNVACTGCL 112
    |||||
Db 61 SLTPAVCHHPALPQDLQPVCSQEQASSIFKTLRTIANDDCELCVNVACTGCL 112
    |||||

RESULT 5
US-10-700-439-145
; Sequence 145, Application US/10700439
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: Bayer Healthcare LLC
; APPLICANT: Burgess, Christopher
; APPLICANT: Myerow, Susan
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Maimonis, Peter
; APPLICANT: Molino, Gary
; APPLICANT: Burtgart, Lawrence
; APPLICANT: Boardman, Lisa A.
; APPLICANT: Thibodeau, Steven
; APPLICANT: Lewis, Marcia
; TITLE OF INVENTION: Use of Differentially Expressed Nucleic Acid Sequences as
; FILE REFERENCE: 1657/2022
; CURRENT APPLICATION NUMBER: US/10/700,439
; CURRENT FILING DATE: 2003-11-04
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; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-439-145

Query Match      100.0%; Score 579; DB 33; Length 112;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGCRAASGLLPQVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLAQWAPSPRLQAQ 60
Db 1 MGCRAASGLLPQVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLAQWAPSPRLQAQ 60

Qy 61 SLLPAVCHHPALPDQLPVCASQSEASSIFKTLRTIANDDCELCVNVACTGCL 112
Db 61 SLLPAVCHHPALPDQLPVCASQSEASSIFKTLRTIANDDCELCVNVACTGCL 112

RESULT 6
US-10-775-481A-56
; Sequence 56, Application US/10775481A
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; APPLICANT: Pitari, Giovanni Mario
; APPLICANT: Park, Jason
; APPLICANT: Schulz, Stephanie
; APPLICANT: Wolfe, Henry R.
; APPLICANT: Lubbe, Wilhelm
; TITLE OF INVENTION: The Use Of GCC Ligands
; FILE REFERENCE: 08321-0168 US1
; CURRENT APPLICATION NUMBER: US/10/775,481A
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/446,730
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-481A-56

Query Match      100.0%; Score 579; DB 33; Length 112;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGCRAASGLLPQVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLAQWAPSPRLQAQ 60
Db 1 MGCRAASGLLPQVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLAQWAPSPRLQAQ 60

Qy 61 SLLPAVCHHPALPDQLPVCASQSEASSIFKTLRTIANDDCELCVNVACTGCL 112
Db 61 SLLPAVCHHPALPDQLPVCASQSEASSIFKTLRTIANDDCELCVNVACTGCL 112

RESULT 7
US-60-453-050-12227
; Sequence 12227, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12227
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-12227

Query Match      100.0%; Score 579; DB 37; Length 112;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGCRAASGLLPQVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLAQWAPSPRLQAQ 60
Db 1 MGCRAASGLLPQVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLAQWAPSPRLQAQ 60

Qy 61 SLLPAVCHHPALPDQLPVCASQSEASSIFKTLRTIANDDCELCVNVACTGCL 112
Db 61 SLLPAVCHHPALPDQLPVCASQSEASSIFKTLRTIANDDCELCVNVACTGCL 112

RESULT 8
US-60-453-135-12227
; Sequence 12227, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12227
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-12227

Query Match      100.0%; Score 579; DB 37; Length 112;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGCRAASGLLPQVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLAQWAPSPRLQAQ 60
Db 1 MGCRAASGLLPQVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLAQWAPSPRLQAQ 60

Qy 61 SLLPAVCHHPALPDQLPVCASQSEASSIFKTLRTIANDDCELCVNVACTGCL 112
Db 61 SLLPAVCHHPALPDQLPVCASQSEASSIFKTLRTIANDDCELCVNVACTGCL 112

RESULT 9
US-60-466-412-12227
; Sequence 12227, Application US/60466412
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001466
; CURRENT APPLICATION NUMBER: US/60/466,412
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 429241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12227
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-466-412-12227

Query Match      100.0%; Score 579; DB 37; Length 112;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGCRAASGLLPQVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLAQWAPSPRLQAQ 60
Db 1 MGCRAASGLLPQVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLAQWAPSPRLQAQ 60

Qy 61 SLLPAVCHHPALPDQLPVCASQSEASSIFKTLRTIANDDCELCVNVACTGCL 112
Db 61 SLLPAVCHHPALPDQLPVCASQSEASSIFKTLRTIANDDCELCVNVACTGCL 112
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Db 1 MGCRAASGLLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSLEAQWAPSPRLQAQ 60
QY 61 SLLPACHHPALPDQLQPVCAQSEASSIFKTLRTIANDDCELCVNVACTGCL 112
Db 61 SLLPACHHPALPDQLQPVCAQSEASSIFKTLRTIANDDCELCVNVACTGCL 112

RESULT 10

US-60-568-073-1020
; Sequence 1020, Application US/60568073
; GENERAL INFORMATION:
; APPLICANT: Huang, Fei
; APPLICANT: Han, Xia
; APPLICANT: Shaw, Peter
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: COLON CANCER BIOMARKERS
; FILE REFERENCE: 10205 PSP
; CURRENT APPLICATION NUMBER: US/60/568,073
; CURRENT FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 1305
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1020
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-568-073-1020

Query Match 100.0%; Score 579; DB 37; Length 112;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGCRAASGLLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSLEAQWAPSPRLQAQ 60
Db 1 MGCRAASGLLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSLEAQWAPSPRLQAQ 60
QY 61 SLLPACHHPALPDQLQPVCAQSEASSIFKTLRTIANDDCELCVNVACTGCL 112
Db 61 SLLPACHHPALPDQLQPVCAQSEASSIFKTLRTIANDDCELCVNVACTGCL 112

RESULT 11

US-60-245-228-223
; Sequence 223, Application US/60245228
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
; FILE REFERENCE: CL000878
; CURRENT APPLICATION NUMBER: US/60/245,228
; CURRENT FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 630
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 122
; TYPE: PRT
; ORGANISM: HUMAN
US-60-245-228-223

Query Match 98.6%; Score 571; DB 37; Length 122;
Best Local Similarity 99.1%; Pred. No. 6e-55;
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGCRAASGLLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSLEAQWAPSPRLQAQ 60
Db 11 MGCRAASGLLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSLEAQWAPSPRLQAQ 70
QY 61 SLLPACHHPALPDQLQPVCAQSEASSIFKTLRTIANDDCELCVNVACTGCL 112
Db 71 SLLPACHHPALPDQLQPVCAQSEASSIFKTLRTIANDDCELCVNVACTGCL 122

RESULT 12

US-60-248-592-71
; Sequence 71, Application US/60248592
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
; FILE REFERENCE: CL000961
; CURRENT APPLICATION NUMBER: US/60/248,592
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 111
; TYPE: PRT
; ORGANISM: HUMAN
US-60-248-592-71

Query Match 97.9%; Score 567; DB 37; Length 111;
Best Local Similarity 99.1%; Pred. No. 1.5e-54;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGCRAASGLLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSLEAQWAPSPRLQAQ 60
Db 1 MGCRAASGLLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSLEAQWAPSPRLQAQ 60
QY 61 SLLPACHHPALPDQLQPVCAQSEASSIFKTLRTIANDDCELCVNVACTGCL 111
Db 61 SLLPACHHPALPDQLQPVCAQSEASSIFKTLRTIANDDCELCVNVACTGCL 111

RESULT 13

US-09-834-366-26398
; Sequence 26398, Application US/09834366
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81.US2.REG
; CURRENT APPLICATION NUMBER: US/09/834,366
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/197,873
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 26398
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-366-26398

Query Match 76.0%; Score 440; DB 23; Length 93;
Best Local Similarity 91.2%; Pred. No. 1.8e-40;
Matches 83; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 22 QSTQSVYIQGFRVQLESMMKLSLEAQWAPSPRLQAQSLPACHHPALPDQLQPVCA 81
Db 3 RGKSKDLKYQGFRVQLESMMKLSLEAQWAPSPRLQAQSLPACHHPALPDQLQPVCA 62
QY 82 SQEASSIFKTLRTIANDDCELCVNVACTGCL 112
Db 63 SQEASSIFKTLRTIANDDCELCVNVACTGCL 93

RESULT 14

US-60-197-873-26398
; Sequence 26398, Application US/60197873
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane

Search completed: March 26, 2005, 17:10:18
Job time : 463.715 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:44:35 ; Search time 34,7445 Seconds
(without alignments)
187.395 Million cell updates/sec

Title: US-10-775-481A-56

Perfect score: 579

Sequence: 1 MGRASGLPGVAVLLLL.....RTIANDCELVCNVACTGCL 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 260697 seqs, 58133403 residues

Total number of hits satisfying chosen parameters: 260697

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New*

- 1: /cgn2_6/ptodata/1/paa/pct_NEW_COMB.pcp.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pcp.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pcp.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pcp.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pcp.*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pcp.*
- 7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pcp.*
- 8: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	16.6	16	7	US-11-066-697-1249
2	74.5	12.9	985	6	US-10-450-763-47493
3	74	12.8	483	6	US-10-450-763-33083
4	73	12.6	351	1	PCT-US04-30360-157
5	71.5	12.3	301	1	PCT-US04-31036-29
6	71.5	12.3	301	1	PCT-US04-31036-31
7	68.5	11.8	166	8	US-60-655-875-165482
8	68.5	11.8	1444	6	US-10-450-763-46026
9	68	11.7	376	7	US-11-031-175-15516
10	68	11.7	1377	1	PCT-US05-02638-105
11	67.5	11.7	819	6	US-10-450-763-49219
12	67.5	11.7	953	7	US-11-031-175-14681
13	67	11.6	187	6	US-10-755-415-236
14	66.5	11.5	228	7	US-11-033-545-409
15	66.5	11.5	393	6	US-10-489-448-1493
16	66.5	11.5	684	6	US-10-450-763-52765
17	66.5	11.5	824	7	US-11-033-545-312
18	66.5	11.5	920	6	US-10-450-763-36280
19	66.5	11.5	920	6	US-10-450-763-52763
20	66.5	11.5	982	6	US-10-450-763-31580
21	66.5	11.5	990	6	US-10-450-763-36281
22	66.5	11.5	990	6	US-10-450-763-52764
23	66.5	11.5	996	6	US-10-450-763-36284
24	66.5	11.5	997	6	US-10-450-763-52766
25	66.5	11.5	1236	6	US-10-450-763-38524

26	66	11.4	776	6	US-10-450-763-58595	Sequence 58595, A
27	65.5	11.3	737	6	US-10-450-763-45465	Sequence 45465, A
28	65.5	11.3	737	6	US-10-489-448-2864	Sequence 2864, Ap
29	64	11.1	315	8	US-60-655-875-131740	Sequence 131740
30	64	11.1	345	6	US-10-491-545A-58	Sequence 58, Appl
31	64	11.1	976	6	US-10-489-448-1519	Sequence 1519, Ap
32	63.5	11.0	122	6	US-10-450-763-50350	Sequence 50350, A
33	63.5	11.0	214	6	US-10-450-763-41255	Sequence 41255, A
34	63.5	11.0	479	1	PCT-US04-17965-1190	Sequence 1190, Ap
35	63.5	11.0	479	1	PCT-US04-17965B-1190	Sequence 1190, Ap
36	63	10.9	269	6	US-10-450-763-43513	Sequence 43513, A
37	63	10.9	353	8	US-60-643-717-8659	Sequence 8659, Ap
38	63	10.9	445	8	US-60-655-875-146849	Sequence 146849, A
39	63	10.9	745	6	US-10-450-763-56461	Sequence 56461, A
40	62.5	10.8	166	8	US-60-655-875-158868	Sequence 158868, A
41	62.5	10.8	608	1	PCT-US05-01983-16	Sequence 16, Appl
42	62.5	10.8	608	1	PCT-US05-01983-90	Sequence 90, Appl
43	62	10.7	114	6	US-10-526-324-1284	Sequence 1284, Ap
44	62	10.7	196	8	US-60-655-875-146820	Sequence 146820, A
45	62	10.7	692	6	US-10-450-763-37251	Sequence 37251, A

ALIGNMENTS

RESULT 1

US-11-066-697-1249
; Sequence 1249, Application US/11066697
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1249
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1249

Query Match 16.6%; Score 96; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 NDDCELVCNVACTGCL 112
Db 1 NDDCELVCNVACTGCL 16

RESULT 2

US-10-450-763-47493
; Sequence 47493, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US

```

; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 03/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 47493
; LENGTH: 985
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (653)..(684)
; OTHER INFORMATION: Protein kinases ATP-binding region proteins domain identified
; OTHER INFORMATION: by eMATRIX, accession number BL00107A, p-value=1.857e-16, raw
; OTHER INFORMATION: score of 18.39
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (521)..(794)
; OTHER INFORMATION: Eukaryotic protein kinase domain identified by PFam,
; OTHER INFORMATION: accession name pkinase, E-value=1e-68, PFam score of 241.7
; US-10-450-763-47493

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Query Match	12.9%	Score	74.5	DB	6	Length	985
Best Local Similarity	24.1%	Pred. NO.	6.4				
Matches	26	Conservative	20	Mismatches	29	Indels	33
Gaps							
Qy	12	GVAVVLLLLLQSTQSVVYIQYGGFVQLDSM-----	KKLSLDEAQWAPSRLOAQ	60			
Db	223	GIACAREI---GNRTVTMESLHMGEIENQITAAFTMGTSLSLSDKCSQFA-----		271			
Qy	61	SLIPAVCHHPALPDLOPVCASQASQASIEFKTLRTIANDDCELCVNVAC	108				
Db	272	--TPSLCHYAF--PYC--DRTSSVPKP-RDLCRDECEILENVLC	308				

```

RESULT 3
US-10-450-763-33083
; Sequence 33083, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 33083
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-33083

```

Query Match	12.8%	Score 74;	DB 6;	Length 483;
Best Local Similarity	26.9%	Pred. No. 3.1;		
Matches	28;	Conservative 10;	Mismatches 36;	Indels 30; Gaps 4;
Qy	7	SGLPGVAVVLLLLQSTQSVVIQYG---	FRVLESKKLSLEAQWAP-----	53
		: :	: :	
		: :	: :	
Db	345	SGTVPR-----	LLQNPGRMDAHSHTLSPRSQTRSGUSQ--EGLMGPARDRCYCHVP	397
		: :	: :	
Qy	54	-----	SPRLQAQSLLPVACHHPALPDQLQFVCASQASS	87
		: :	: :	

Db 398 PLNFCPNMHKAPRACAVSALRVLC THPPT SAGLSPNC SHLQLSS 441

```

RESULT 4
PCT-US04-30360-157
; Sequence 157, Application PC/TUS0430360
; GENERAL INFORMATION:
; APPLICANT: PLEXIKON, INC.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1703
; CURRENT APPLICATION NUMBER: PCT/US04/30360
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 157
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
PCT-US04-30360-157

```

	Query Match	12.68;	Score 73;	DB 1;	Length 351;
	Best Local Similarity	32.09;	Pred. No. 2.7;		
	Matches 24;	Conservative	16;	Mismatches	25; Indels 10; Gaps 4;
Qy	41	MKKLSLEAQWAPSFRLOAQSLLPAVCHHPAL---	PQOLQPVCASQEAASSFKYRTTAND	98	
	:	: :	:	:	:
	:	: :	:	:	:
Db	274	MRELIEASLRNPNHRPRAADL----	KHEALNPFPREDQPRCTSLD--SALLERKRLLSRK	328	
	:	: :	:	:	:
	:	: :	:	:	:
Qy	99	DCELCVNVA---CTG	110		
	:	:	:	:	:
	:	:	:	:	:
Db	329	EELPENIADSSTCG	343		

```

RESULT 5
PCT-US04-31036-29
; Sequence 29, Application PC/TUS0431036
; GENERAL INFORMATION:
; APPLICANT: Dale Umetsu
; APPLICANT: Rosemarie DeKruyff
; APPLICANT: Jennifer McIntire
; APPLICANT: Gordon Freeman
; TITLE OF INVENTION: T CELL REGULATORY GENES ASSOCIATED WITH
; TITLE OF INVENTION: IMMUNE DISEASE
; FILE REFERENCE: STAN-235CIP
; CURRENT APPLICATION NUMBER: PCT/US04/31036
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/188,012
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 301
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(301)
; OTHER INFORMATION: TIM-3, allele 1
PCT-US04-31036-29

```

```
Query Match      12.3%; Score 71.5; DB 1; Length 301;
Best Local Similarity 28.0%; Pred.No. 3.4;
Matches 26; Conservative 12; Mismatches 28; Indels 27; Gaps 3
Qy              10 LPGVAVNLLLLLQSTQSYIYIQYGRFRVOLESMKKLSDLQAQWSPRIQAQSLLIPAVCHH 69
```



```
Db 5 LPFDCVLLLLLLLTSRSEVEYRA-----EVGQNAVLPYCF-YT 41
Qy 70 PALPDLOPVCAQASQASIFK-----TLRTIAND 98
Db 42 PAAPGNLVPVCGKACPVFCGNNVLTDERD 74

RESULT 6
PCT-US04-31036-31
; Sequence 31, Application PC/TUS0431036
; GENERAL INFORMATION:
; APPLICANT: Dale Umetsu
; APPLICANT: Rosemarie Dekruyff
; APPLICANT: Jennifer McIntire
; APPLICANT: Gordon Freeman
; TITLE OF INVENTION: T CELL REGULATORY GENES ASSOCIATED WITH
; TITLE OF INVENTION: IMMUNE DISEASE
; FILE REFERENCE: STAN-235CIP
; CURRENT APPLICATION NUMBER: PCT/US04/31036
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/188,012
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 301
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(301)
; OTHER INFORMATION: TIM-3, allele 2
PCT-US04-31036-31

Query Match 12.3%; Score 71.5; DB 1; Length 301;
Best Local Similarity 28.0%; Pred. No. 3.4;
Matches 26; Conservative 12; Mismatches 28; Indels 27; Gaps 3;

Qy 10 LPGVAVVLLLLQSTQSVIYQGFVQVLESMKKSLDLAQWAPSPRLQAOSSLPAVCHH 69
Db 5 LPFDCVLLLLLLLTSRSEVEYRA-----EVGQNAVLPYCF-YT 41
Qy 70 PALPDLOPVCAQASQASIFK-----TLRTIAND 98
Db 42 PAAPGNLVPVCGKACPVFCGNNVLTDERD 74

RESULT 7
US-60-655-875-165482
; Sequence 165482, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijing
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETEROERA INFESTATIONS
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 165482
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Heterodera glycines
```

```
; FEATURE:
; OTHER INFORMATION: Coding regions on vDNA: vDNA=SeqID_91905; Strand=+; Position=2-
US-60-655-875-165482

Query Match 11.8%; Score 68.5; DB 8; Length 166;
Best Local Similarity 24.0%; Pred. No. 3.6;
Matches 25; Conservative 19; Mismatches 41; Indels 19; Gaps 4;

Qy 21 LQSTQSVIYQGFVQVLESMKKSLDLAQWAPSPRLQAOSSLPAVCHHHPALPD 75
Db 48 LQKKSLHLSPRGTKSTHFSNEREAQKQPKTKRRPQTTK--BRDALTKIHAQKLTQQ 105
Qy 76 LQPVCAQASQASQASIFK-----IFKTIARTIANDDCELCVNVACTG 110
Db 106 LRRVQSDWESASVMVLRREGDAVVVKALR---QDGFSLCDNAVSSG 146

RESULT 8
US-10-450-763-46026
; Sequence 46026, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 46026
; LENGTH: 1444
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (996)...(1012)
; OTHER INFORMATION: Kw ANNEXIN ANTIGEN PROLINE TUMOR domain identified by
; OTHER INFORMATION: EMATRIX, accession number DM00250A, p-value=6.211e-10, raw score
; OTHER INFORMATION: 10.52
US-10-450-763-46026

Query Match 11.8%; Score 68.5; DB 6; Length 1444;
Best Local Similarity 31.4%; Pred. No. 47;
Matches 32; Conservative 9; Mismatches 46; Indels 15; Gaps 4;

Qy 4 RAASGLLPGVAVVLLLLQSTQSVIYQGFVQVLESMKKSLDLAQWAPSPRLQAOSSLPAVCHHHPALPD 54
Db 1036 RARSGLOPQPPAVLSLLGSAQ---VPOQG--VLPVSLVQQQPPQPPKLLQLPQWQPK 1090
Qy 55 PRL-QAOSLLPAVCHHHPALPDLOPVCAQASQASIFKTLRTI 95
Db 1091 PRDEPQSQQQPQHILQTLQRLVLPQPHILQTLQTLQRLV 1132

RESULT 9
US-11-031-175-15516
; Sequence 15516, Application US/11031175
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/11/031,175
; CURRENT FILING DATE: 2005-01-08
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
```



```
; APPLICANT: DASH, DEBASIS
; APPLICANT: SHARMA, RAWAKANT
; APPLICANT: MAHESHWARI, JITENDRA KUMAR
; TITLE OF INVENTION: A COMPUTER BASED VERSATILE METHOD FOR IDENTIFYING PROTEIN CODING
; TITLE OF INVENTION: DNA SEQUENCES USEFUL AS DRUG TARGETS
; FILE REFERENCE: 026033-00029
; CURRENT APPLICATION NUMBER: US/10/755,415
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: 10/727,989
; PRIOR FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 236
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-755-415-236

Query Match 11.6%; Score 67; DB 6; Length 187;
Best Local Similarity 31.0%; Pred. No. 6;
Matches 18; Conservative 7; Mismatches 21; Indels 12; Gaps 2;

Qy 50 QWAPSPR---LQAQSLP-----VCHHPALPQDLQPCASQEAASSIFKTLRTI 95
Db 110 RMWSPRVAIRAAALMALPATAIRLSMQGICTSPAMGSQVRPLCSMAISAAPSTCRGV 167

RESULT 14
US-11-033-545-409
; Sequence 409, Application US/11033545
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/11/033,545
; CURRENT FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 409
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Human
US-11-033-545-409

Query Match 11.5%; Score 66.5; DB 7; Length 228;
Best Local Similarity 32.0%; Pred. No. 8.7;
Matches 32; Conservative 12; Mismatches 35; Indels 21; Gaps 5;

Qy 5 AASGLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSLEAQAQWAPSPRL----- 57
Db 104 AASGLPVLVVVLLVLL---AVLVTLAGITVYRKARSRI--LSRNVAPKTTMGSRNPLF 158

Qy 58 -QAQSLPAPVCHHPAL---PQDLQPC-----ASQEAASSI 88
Db 159 HQAASRPVPAKGAPAPSGPQELVPTTHPGQPARHPASSV 198

RESULT 15
US-10-489-448-1493
; Sequence 1493, Application US/10489448
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
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; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Ma, Yunqing
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radjef T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 810CIP PCT
; CURRENT APPLICATION NUMBER: US/10/489,448
; CURRENT FILING DATE: 1004-03-10
; PRIOR APPLICATION NUMBER: US 60/324,631
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3476
; SOFTWARE: pt-FL Genes Version 6.0
; SEQ ID NO 1493
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-489-448-1493

Query Match 11.5%; Score 66.5; DB 6; Length 393;
Best Local Similarity 24.0%; Pred. No. 17;
Matches 24; Conservative 8; Mismatches 35; Indels 33; Gaps 2;

Qy 3 CRAAGLLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSLE----- 48
Db 242 CEVLKEVIGVVIETLDLVLET-----FRKSLRGQKMLPLLSQRRFVLLHNGEADP 292

Qy 49 -----AQAAPSRLQAQSLPAPVCHHPALPQDLQ 78
Db 293 RPHLGSCSLRRPPLPPLTRQAKSGGPPMPHAPDQPGARRP 332

Search completed: March 26, 2005, 17:11:53
Job time : 34.7445 secs
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:49:45 ; Search time 84.4821 Seconds
(without alignments)
86.982 Million cell updates/sec

Title: US-10-775-481A-2

Perfect score: 19
Sequence: 1 NNTFYCELCCNPACAGCY 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	2	AAR85946
2	19	100.0	19	2	AAY40508
3	19	100.0	19	8	ADR45822
4	19	100.0	72	8	ADR48355
5	18	94.7	18	2	AAR85956
6	18	94.7	18	2	AAR85950
7	18	94.7	18	2	AAY40543
8	18	94.7	18	2	AAY40518
9	18	94.7	18	2	AAY40512
10	18	94.7	18	2	AAY02385
11	18	94.7	18	2	AAY29607
12	18	94.7	18	2	AAY02397
13	18	94.7	18	8	ADR48330
14	18	94.7	18	8	ADR48332
15	18	94.7	18	8	ADR48341
16	18	94.7	18	8	ADR45832
17	18	94.7	18	8	ADR45857
18	18	94.7	18	8	ADR45826
19	18	94.7	36	1	AAP30262
20	17	89.5	17	2	AAR85951
21	17	89.5	17	2	AAR85957
22	17	89.5	17	2	AAY40519
23	17	89.5	17	2	AAY40546
24	17	89.5	17	2	AAY40513
25	17	89.5	17	8	ADR45827

26	17	89.5	17	8	ADR45833	AAR45833 Amino aci
27	17	89.5	17	8	ADR45860	AAR45860 Amino aci
28	17	89.5	18	2	AAY06971	AAY06971 E. coli h
29	16	84.2	16	2	AAR85952	AAR85952 ST Ia rec
30	16	84.2	16	2	AAR85958	AAR85958 ST Ia rec
31	16	84.2	16	2	AAY40514	AAY40514 ST recept
32	16	84.2	16	2	AAY40520	AAY40520 ST recept
33	16	84.2	16	8	ADR45834	ADR45834 Amino aci
34	16	84.2	16	8	ADR45828	ADR45828 Amino aci
35	15	78.9	15	2	AAR85959	AAR85959 ST Ia rec
36	15	78.9	15	2	AAR85953	AAR85953 ST Ia rec
37	15	78.9	15	2	AAY40515	AAY40515 ST recept
38	15	78.9	15	2	AAY40547	AAY40547 ST recept
39	15	78.9	15	2	AAY40521	AAY40521 ST recept
40	15	78.9	15	8	ADR45829	ADR45829 Amino aci
41	15	78.9	15	8	ADR45835	ADR45835 Amino aci
42	15	78.9	15	8	ADR45861	ADR45861 Amino aci
43	15	78.9	18	8	ADR48342	ADR48342 Bacterial
44	14	73.7	14	2	AAR85960	AAR85960 ST Ia rec
45	14	73.7	14	2	AAR85954	AAR85954 ST Ia rec

ALIGNMENTS

RESULT 1
AAR85946
ID AAR85946 standard; peptide; 19 AA.
XX
AC AAR85946;
XX
DT 19-JAN-1996 (first entry)
XX
DE ST Ia receptor ligand portion.
XX
KW ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
KW colorectal; metastasis.
XX
OS Escherichia coli.
XX
PN WO9511694-A1.
XX
PD 04-MAY-1995.
XX
PF 26-OCT-1994; 94WO-US012232.
XX
PR 26-OCT-1993; 93US-00141892.
PR 13-SEP-1994; 94US-00305056.
XX
(UYJE-) UNIV JEFFERSON THOMAS.
Waldman SA;
XX
DR WPI; 1995-1786646/23.
XX
PT Conjugated cpds. which specifically bind to colorectal cancer cells -
PT comprise heat-stable toxin receptor binding moiety and active moiety
PT which may be a therapeutic agent or a radioactive agent.
XX
PS Claim 3; Page 116; 133pp; English.
XX
CC New conjugated compounds are provided which consist of (1) an ST receptor
CC binding moiety and (2) an active moiety which is a radio- stable agent.
CC 'ST' refers to a heat stable toxin produced by E.coli and other
CC organisms. Especially the radiostable agent is a therapeutic agent (e.g.
CC methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive
CC isotope) or nucleic acid; and the compound is used for the detection,
CC imaging or treatment of colorectal tumours, particularly metastasised
CC tumours. The present sequence is a specific example of an ST receptor
XX binding peptide which can be used in the conjugate
SQ Sequence 19 AA;

Query Match 100.0%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e-13; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNTFYCCCLCCNPACAGCY 19
DB 1 NNTFYCCCLCCNPACAGCY 19

RESULT 2
AAY40508
ID AAY40508 standard; peptide; 19 AA.
XX
AC AAY40508;
XX
DT 03-DEC-1999 (first entry)
XX
DE ST receptor peptide ST 1a.
XX
KW Conjugated compound; ST receptor; heat-stable; toxin; colorectal cancer.
XX
OS Escherichia coli.
XX
XX
PN US5962220-A.
XX
PD 05-OCT-1999.
XX
XX 06-JUN-1995; 95US-00467920.
XX
XX 26-OCT-1993; 93US-00141892.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Waldman SA;
XX
XX WPI; 1999-571264/48.
DR N-PSDB; AAZ07540.
XX
XX Conjugated compound comprising a receptor moiety and active moiety,
PT useful for the treatment/prevention of colorectal cancer.
XX
XX Claim 1; Col 19-20; 23pp; English.
XX
XX The invention relates to a conjugated compound that comprises a ST (heat-
CC stable toxin) receptor moiety selected from one of the sequences shown in
CC AAY40508-Y40559 and an active moiety (antisense molecule). The compound
CC is useful for the treatment of colorectal cancer. The use of the
CC conjugated compound is advantageous compared to antibodies since it binds
CC specifically to colorectal cells and has no toxic effect on normal cells.
CC The present sequence represents the amino acid sequence of a ST receptor
CC peptide ST 1a
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNTFYCCCLCCNPACAGCY 19
DB 1 NNTFYCCCLCCNPACAGCY 19

RESULT 3
ADR45822
ID ADR45822 standard; peptide; 19 AA.
XX
AC ADR45822;
XX
DT 18-NOV-2004 (first entry)
XX
XX Amino acid sequence of heat stable toxin ST 1a.
DE
XX

KW heat stable toxin; ST; ST receptor; colorectal cancer; gastric cancer;
KW oesophageal cancer; colorectal cell; gastric cell; oesophageal cell;
XX ST 1a.
OS Unidentified.
XX
PN WO2004071436-A2.
XX
PD 26-AUG-2004.
XX
PF 10-FEB-2004; 2004WO-US003765.
XX
PR 10-FEB-2003; 2003US-0446730P.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Waldman SA, Pitari GM, Park J, Schulz S, Wolfe HR,
PI
DR WPI; 2004-615913/59.
XX N-PSDB; ADR45821.
XX
PT Increasing ST receptor molecules on the surface of a colorectal, gastric
PT or esophageal cancer cell to treat these cancers comprises administering
PT ST receptor ligand molecules that bind to ST receptors on the surface of
PT the cancer cell.
XX
PS Claim 6; SEQ ID NO 2; 97pp; English.
XX
XX The specification describes a method for increasing the number of heat
CC stable toxin (ST) receptor molecules on the surface of a metastasised
CC colorectal cancer cell. The method comprises administering, by continuous
CC infusion, at least 0.1 nM of an ST receptor ligand per 10 kg bodyweight
CC per hour for at least 6 hours, where ST receptor ligand molecules bind to
CC ST receptors on the surface of the cancer cell in the individual and the
CC number of ST receptor molecules on the surface of the cancer cell is
CC increased. Therapeutic compositions comprising components which target ST
CC receptors can then be used to inhibit proliferation of the colorectal,
CC gastric and oesophageal cells. This method may be used for treating
CC individuals that have diseases that affect colorectal, gastric and
CC oesophageal cells, including colorectal, gastric or oesophageal cancers.
CC The present sequence represents a ST, designated ST 1a, which is used as
CC the ST receptor ligand in the method of the invention.
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNTFYCCCLCCNPACAGCY 19
DB 1 NNTFYCCCLCCNPACAGCY 19

RESULT 4
ADR48355
ID ADR48355 standard; peptide; 72 AA.
XX
AC ADR48355;
XX
DT 04-NOV-2004 (first entry)
XX
XX Immature E. coli ST-1A peptide.
XX
XX Gastrointestinal; antiinflammatory; laxative; cardiant; antilucer;
KW anorectic; cardiovascular; cytostatic; analgesic; CNS; respiratory;
KW neuroprotective; vasotropic; auditory; antiemetic; antiasthmatic;
KW nephrotropic; hepatotropic; virucide; immunosuppressive; antiallergic;
KW antidiabetic; ophthalmological; tranquiliser; hypnotic; nootropic;
KW guanilate cyclase C; GC-C; receptor; gastrointestinal disorder;
KW irritable bowel syndrome; constipation; gastroesophageal reflux disease;
KW heartburn; dyspepsia; gastroparesis; Crohn's disease; ulcerative colitis;
KW inflammatory bowel disease; obesity; heart failure; cystic fibrosis;
KW

KW cancer; respiratory disorder; neurological disorder; carbonate imbalance;
 KW erectile dysfunction; inner ear disorder; slow digestion; nausea;
 KW vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy;
 KW retinopathy; nephropathy; headache; anxiety; sleep disorder.

XX Escherichia coli.

XX WO2004069165-A2.

XX 19-AUG-2004.

XX 28-JAN-2004; 2004WO-US002390.

XX 28-JAN-2003; 2003US-0443098P.

XX 15-MAY-2003; 2003US-0471288P.

XX 12-NOV-2003; 2003US-0519460P.

XX (MICR-) MICROBIA INC.

XX Currie MG, Mahajan-Miklos S;

XX WPI; 2004-604332/58.

XX Novel purified peptide capable of activating the guanylate cyclase C
 receptor, useful for treating obesity, congestive heart failure and
 benign prostatic hyperplasia.

XX Disclosure; Page 30; 93pp; English.

XX The invention relates to a purified peptide (P1) capable of activating
 the guanylate cyclase C (GC-C) receptor. Further disclosed is a
 pharmaceutical composition comprising the peptide of the invention. The
 composition of the invention is useful for treating a gastrointestinal
 disorder in a patient, which involves administering P1, where the
 gastrointestinal disorder is gastrointestinal motility disorder,
 irritable bowel syndrome, chronic constipation, a functional
 gastrointestinal disorder, gastroesophageal reflux disease, functional
 heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
 gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
 obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel
 disease. The peptide of the invention is also useful for treating
 obesity, congestive heart failure, cystic fibrosis or a patient suffering
 from constipation. The P1/GC-C receptor agonist is useful for treating
 cancer, respiratory disorder, neurological disorder, disorder associated
 with carbonate imbalance, erectile dysfunction, insulin-related disorder
 or inner ear disorder. P1 is useful in treating slow digestion or slow
 stomach emptying. P1 is useful in relieving symptoms of gastroparesis,
 such as nausea, vomiting, bloating, and delayed gastric emptying. P1 is
 useful for treating or preventing asthma, nephritis, hepatitis,
 pancreatitis, allergies, etc. P1 is useful for treating or preventing
 type II diabetes mellitus, hyperglycaemia, respiratory disorders
 including inhalation. P1 is useful in treating or preventing retinopathy,
 nephropathy and edema formation. P1 is useful for treating or preventing
 headache, anxiety, sleep disorders and memory loss. P1 is useful as a
 marker to identify, detect, stage, or diagnosis diseases and conditions
 of the small intestine, including Crohn's disease, colitis, inflammatory
 bowel disease, tumours, etc. P1 can be conjugated to diagnostic or
 therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
 fibrosis lesions and specific cells lining the intestinal tract, thus
 useful in targeting radioactive moieties or therapeutic moieties to the
 intestine to aid in imaging and diagnosing or treating
 colorectal/metastatic or local colorectal cancer. The current sequence
 represents a bacterial ST peptide which is an activator of the GC-C
 receptor. ST peptides are considered super agonists of GC-C and are very
 resistant to proteolytic degradation.

XX Sequence 72 AA;

Query Match 100.0%; Score 19; DB 8; Length 72;
 Best Local Similarity 100.0%; Pred. No. 2.9e-13;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NNTFYCCCLCCNPACAGCY 19

Db 54 NNTFYCCCLCCNPACAGCY 72

RESULT 5
 AAR85956

ID AAR85956 standard; peptide; 18 AA.

XX AAR85956;

XX 19-JAN-1996 (first entry)

XX ST Ia receptor ligand portion.

XX ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
 colorectal; metastasis.

XX Escherichia coli.

XX WO9511694-A1.

XX 04-MAY-1995.

XX 26-OCT-1994; 94WO-US012232.

XX 26-OCT-1993; 93US-00141892.

XX 13-SEP-1994; 94US-00305056.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Waldman SA;

XX WPI; 1995-178646/23.

XX Conjugated cpds. which specifically bind to colorectal cancer cells -
 comprise heat-stable toxin receptor binding moiety and active moiety
 which may be a therapeutic agent or a radioactive agent.

XX Claim 3; Page 118; 133pp; English.

XX New conjugated compounds are provided which consist of (1) an ST receptor
 binding moiety and (2) an active moiety which is a radio-stable agent.
 'ST' refers to a heat stable toxin produced by E.coli and other
 organisms. Especially the radiostable agent is a therapeutic agent (e.g.
 methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive
 isotope) or nucleic acid; and the compound is used for the detection,
 imaging or treatment of colorectal tumours, particularly metastasised
 tumours. The present sequence is a specific example of an ST receptor
 binding peptide which can be used in the conjugate

XX Sequence 18 AA;

Query Match 94.7%; Score 18; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 NNTFYCCCLCCNPACAGCY 19

Db 1 NNTFYCCCLCCNPACAGCY 18

RESULT 6
 AAR85950

ID AAR85950 standard; peptide; 18 AA.

XX AAR85950;

XX 19-JAN-1996 (first entry)

XX ST Ia receptor ligand portion.

XX ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
 colorectal; metastasis.

RESULT 9
 AAY40512
 ID AAY40512 standard; peptide; 18 AA.
 XX
 AC AAY40512;
 DT 03-DEC-1999 (first entry)
 XX ST receptor binding peptide.
 DE
 XX Conjugated compound; ST receptor; heat-stable; toxin; colorectal cancer.
 KW Escherichia coli.
 XX
 OS USS962220-A.
 XX
 PN 05-OCT-1999.
 XX
 PD 06-JUN-1995; 95US-00467920.
 XX
 PF 26-OCT-1993; 93US-00141892.
 XX
 PR (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PA Waldman SA;
 XX
 PI WPI; 1999-571264/48.
 XX
 DR Conjugated compound comprising a receptor moiety and active moiety,
 XX useful for the treatment/prevention of colorectal cancer.
 PT
 XX Claim 1; Col 21-22; 23pp; English.
 PS
 XX The invention relates to a conjugated compound that comprises a ST (heat-
 CC stable toxin) receptor moiety selected from one of the sequences shown in
 CC AAY40508-Y40559 and an active moiety (antitense molecule). The compound
 CC is useful for the treatment of colorectal cancer. The use of the
 CC conjugated compound is advantageous compared to antibodies since it binds
 CC specifically to colorectal cells and has no toxic effect on normal cells
 XX
 SQ Sequence 18 AA;
 Query Match 94.7%; Score 18; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NNTFYCCELCNCPACAGC 18
 Db 1 NNTFYCCELCNCPACAGC 18
 RESULT 10
 AAY02385
 ID AAY02385 standard; peptide; 18 AA.
 XX
 AC AAY02385;
 DT 09-JUL-1999 (first entry)
 XX Heat stable ST enterotoxin Sta.
 DE
 XX Selection; candidate drug; cell receptor binding; affinity;
 KW biological receptor; rational drug design; combinatorial drug design;
 KW receptor antagonist; receptor agonist; ST enterotoxin; beta turn mimetic;
 KW gamma-turn mimetic; beta sheet mimetic; disulphide bridge mimetic.
 XX
 OS Escherichia coli.
 XX
 PN WO9909416-A2.
 XX
 PD 25-FEB-1999.
 XX
 PS
 Query Match 94.7%; Score 18; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NNTFYCCELCNCPACAGC 18
 Db 1 NNTFYCCELCNCPACAGC 18
 RESULT 11
 AAY29607
 ID AAY29607 standard; peptide; 18 AA.
 XX
 AC AAY29607;
 DT 15-OCT-1999 (first entry)
 XX Escherichia coli heat stable ST enterotoxin Sta.
 DE
 XX Heat stable ST enterotoxin; immunoreagent; radiological therapy;
 KW diagnosis; ST receptor binding moiety; macrocyclic complexing agent;
 KW tumour; infectious diarrhoeal disease; diarrhoea.
 XX
 OS Escherichia coli.
 XX
 PN WO9939748-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 08-FEB-1999; 99WO-GB000396.
 XX
 PR 06-FEB-1998; 98US-00020233.
 XX
 XX (NYCO-) NYCOMED IMAGING AS.
 PA (MATY) MATTHEWS D P.
 XX
 PI Snow RA, Delecki DJ, Shah C, Black C, Wolfe H;
 XX WPI; 1999-494219/41.
 DR
 XX Macrocyclic complexing agents containing linked 2,6-pyridinylene nuclei
 PT as components of targeting immunoreagents binding to ST receptor.
 XX
 PS Disclosure; Page 39; 79pp; English.

XX The present invention describes targeting immunoreagents (TI's)
 CC comprising a metal ion and a residue of a macrocyclic complexing agent
 CC (MCA). TI's are of use in diagnostic imaging and therapy of specific
 CC disease sites in a patient, using either radioactive, magnetic resonance,
 CC or fluorescent means of detection or use of the metal ion; alternatively,
 CC a substituent of these types may be introduced, e.g. radioactive iodine,
 CC to perform the same function. Most notable is the imaging and
 CC radiological therapy of tumours. In addition, a variety of bacteria,
 CC including *Escherichia coli*, *Vibrio cholerae*, *Citrobacter freundii*, and
 CC *Yersinia enterocolitica*, bind to ST receptors and cause infectious
 CC diarrhoeal diseases, particularly in pediatrics and in developing
 CC countries. These types of diarrhoea can also be treated using TI's. TI's
 CC may specifically used to treat cancers and also be used as an
 CC anti-diarrhoeal agent. TI's are free from the various disadvantages of
 CC prior art reagents, including rapid destruction and/or excretion,
 CC instability in storage, and protein degradation. There is no perturbation
 CC of protein reactive groups at the pyridyl chelating site. AAY29607 to
 CC AAY29612 represent examples of heat stable ST enterotoxins given in the
 CC exemplification of the present invention
 XX Sequence 18 AA;
 SQ

Query Match 94.7%; Score 18; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCELCCNPACAGCY 19
 DB 1 NTFYCCELCCNPACAGCY 18
 |||||

RESULT 12

RAY02397
 ID AAY02397 standard; peptide; 18 AA.

AC RAY02397;
 DT 09-JUL-1999 (first entry)
 XX Heat stable ST enterotoxin Sta.

XX Selection; candidate drug; cell receptor binding; affinity;
 KW biological receptor; rational drug design; combinatorial drug design;
 KW receptor antagonist; receptor agonist; ST enterotoxin; beta turn mimetic;
 KW gamma-turn mimetic; beta sheet mimetic; disulphide bridge mimetic.

XX *Escherichia coli*.

XX WO9909417-A2.

XX 25-FEB-1999.

XX 20-AUG-1998; 98WO-GB002510.

XX 20-AUG-1997; 97GB-00017652.

XX (NYCO-) NYCOMED IMAGING AS.

PA (COCK/) COCKBAIN J.

XX Wolfe HR;

XX WPI; 1999-181157/15.

XX Method of drug selection - using a combination of rational and
 PT combinatorial drug design techniques.

XX Disclosure; Page 1; 35pp; English.

XX The specification describes a method for selecting a candidate drug
 CC compound having affinity for biological receptors. The method uses a
 CC combination of rational and combinatorial drug design techniques. At
 CC least 1 residue in the original cell receptor binding peptide is modified

CC to a non-natural amino acid, preferably a beta turn mimetic, a gamma-turn
 CC mimetic, a beta sheet mimetic or a disulphide bridge mimetic. The method
 CC is used for identification of a candidate receptor antagonist or agonist.
 CC The present peptide is a cell receptor binding peptide, and can thus be
 CC used as a starting point for identification of candidate drug compounds,
 CC using the method of the invention

XX Sequence 18 AA;

Query Match 94.7%; Score 18; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCELCCNPACAGCY 19
 DB 1 NTFYCCELCCNPACAGCY 18
 |||||

RESULT 13

ADR48330
 ID ADR48330 standard; peptide; 18 AA.

XX ADR48330;

XX 04-NOV-2004 (first entry)

XX *E. coli* ST Ia peptide.

XX Gastrointestinal; antiinflammatory; laxative; cardiant; antiulcer;
 KW anorectic; cardiovascular; cytostatic; analgesic; CNS; respiratory;
 KW neuroprotective; vasotropic; auditory; antiemetic; antiasthmatic;
 KW nephrotropic; hepatotropic; virucide; immunosuppressive; antiallergic;
 KW antidiabetic; ophthalmological; tranquiliser; hypnotic; nootropic;
 KW guanylate cyclase C; GC-C; receptor; gastrointestinal disorder;
 KW irritable bowel syndrome; constipation; gastroesophageal reflux disease;
 KW heartburn; dyspepsia; gastroparesis; Crohn's disease; ulcerative colitis;
 KW inflammatory bowel disease; obesity; heart failure; cystic fibrosis;
 KW cancer; respiratory disorder; neurological disorder; carbonate imbalance;
 KW erectile dysfunction; inner ear disorder; slow digestion; nausea;
 KW vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy;
 KW retinopathy; nephropathy; headache; anxiety; sleep disorder.

XX *Escherichia coli*.

XX WO2004069165-A2.

XX 19-AUG-2004.

XX 28-JAN-2004; 2004WO-US002390.

XX 28-JAN-2003; 2003US-0443098P.

PR 15-MAY-2003; 2003US-0471288P.

PR 12-NOV-2003; 2003US-0519460P.

XX (MICR-) MICROBIA INC.

XX Currie MG, Mahajan-Miklos S;

XX WPI; 2004-604332/58.

XX Novel purified peptide capable of activating the guanylate cyclase C
 PT receptor, useful for treating obesity, congestive heart failure and
 PT benign prostatic hyperplasia.

XX Disclosure; Page 28; 93pp; English.

XX The invention relates to a purified peptide (PI) capable of activating
 CC the guanylate cyclase C (GC-C) receptor. Further disclosed is a
 CC pharmaceutical composition comprising the peptide of the invention. The
 CC composition of the invention is useful for treating a gastrointestinal
 CC disorder in a patient, which involves administering PI, where the
 CC gastrointestinal disorder is gastrointestinal motility disorder,
 CC irritable bowel syndrome, chronic constipation, a functional

CC gastrointestinal disorder, gastroesophageal reflux disease, functional
 CC heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
 CC gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
 CC obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel
 CC disease. The peptide of the invention is also useful for treating
 CC obesity, congestive heart failure, cystic fibrosis or a patient suffering
 CC from constipation. The P1/GC-C receptor agonist is useful for treating
 CC cancer, respiratory disorder, neurological disorder, disorder associated
 CC with carbonate imbalance, erectile dysfunction, insulin-related disorder
 CC or inner ear disorder. P1 is useful in treating slow digestion or slow
 CC stomach emptying. P1 is useful in relieving symptoms of gastroparesis
 CC such as nausea, vomiting, bloating, and delayed gastric emptying. P1 is
 CC useful for treating or preventing asthma, nephritis, hepatitis,
 CC pancreatitis, allergies, etc. P1 is useful for treating or preventing
 CC type II diabetes mellitus, hyperglycemia, respiratory disorders
 CC including inhalation. P1 is useful in treating or preventing retinopathy,
 CC nephropathy and edema formation. P1 is useful for treating or preventing
 CC headache, anxiety, sleep disorders and memory loss. P1 is useful as a
 CC marker to identify, detect, stage, or diagnosis diseases and conditions
 CC of the small intestine, including Crohn's disease, colitis, inflammatory
 CC bowel disease, tumours, etc. P1 can be conjugated to diagnostic or
 CC therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
 CC fibrosis lesions and specific cells lining the intestinal tract, thus
 CC useful in targeting radioactive moieties or therapeutic moieties to the
 CC intestine to aid in imaging and diagnosing or treating
 CC colorectal/metastasised or local colorectal cancer. The current sequence
 CC represents a bacterial ST peptide which is an activator of the GC-C
 CC receptor. ST peptides are considered super agonists of GC-C and are very
 CC resistant to proteolytic degradation.

XX Sequence 18 AA;

Query Match 94.7%; Score 18; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 NTFYCCCLCCNPACAGCY 19

Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 14

ADR48332 94.7%; Score 18; DB 8; Length 18;
 ID ADR48332 standard; peptide; 18 AA.

XX AC ADR48332;

XX DT 04-NOV-2004 (first entry)

XX DE C. freundii ST peptide.

XX Gastrointestinal; antiinflammatory; laxative; cardiant; antiulcer;
 KW anorectic; cardiovascular; cytostatic; analgesic; CNS; respiratory;
 KW neuroprotective; vasotropic; auditory; antileptic; antiasthmatic;
 KW nephrotropic; hepatotropic; virucide; immunosuppressive; antiallergic;
 KW antididiabetic; ophthalmological; tranquiliser; hypnotic; nootropic;
 KW guanylate cyclase C; GC-C; receptor; gastrointestinal disorder;
 KW irritable bowel syndrome; constipation; gastroesophageal reflux disease;
 KW heartburn; dyspepsia; gastroparesis; Crohn's disease; ulcerative colitis;
 KW inflammatory bowel disease; obesity; heart failure; cystic fibrosis;
 KW cancer; respiratory disorder; neurological disorder; carbonate imbalance;
 KW erectile dysfunction; inner ear disorder; slow digestion; nausea;
 KW vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy;
 KW retinopathy; nephropathy; headache; anxiety; sleep disorder.

XX Citrobacter freundii.

XX OS WO2004069165-A2.

XX PN 19-AUG-2004.

XX PD 28-JAN-2004; 2004WO-US002390.

XX PF

PR 28-JAN-2003; 2003US-0443098P.

PR 15-MAY-2003; 2003US-0471288P.

XX PR 12-NOV-2003; 2003US-0519460P.

XX PA (MICR-) MICROBIA INC.

XX PI Currie MG, Mahajan-Miklos S;

XX WPI; 2004-604332/58.

XX Novel purified peptide capable of activating the guanylate cyclase C
 PT receptor, useful for treating obesity, congestive heart failure and
 PT benign prostatic hyperplasia.

XX Disclosure; Page 28; 93pp; English.

XX The invention relates to a purified peptide (P1) capable of activating
 CC the guanylate cyclase C (GC-C) receptor. Further disclosed is a
 CC pharmaceutical composition comprising the peptide of the invention. The
 CC composition of the invention is useful for treating a gastrointestinal
 CC disorder in a patient, which involves administering P1, where the
 CC gastrointestinal disorder is gastrointestinal motility disorder,
 CC irritable bowel syndrome, chronic constipation, a functional
 CC gastrointestinal disorder, gastroesophageal reflux disease, functional
 CC heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
 CC gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
 CC obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel
 CC disease. The peptide of the invention is also useful for treating
 CC obesity, congestive heart failure, cystic fibrosis or a patient suffering
 CC from constipation. The P1/GC-C receptor agonist is useful for treating
 CC cancer, respiratory disorder, neurological disorder, disorder associated
 CC with carbonate imbalance, erectile dysfunction, insulin-related disorder
 CC or inner ear disorder. P1 is useful in treating slow digestion or slow
 CC stomach emptying. P1 is useful in relieving symptoms of gastroparesis
 CC such as nausea, vomiting, bloating, and delayed gastric emptying. P1 is
 CC useful for treating or preventing asthma, nephritis, hepatitis,
 CC pancreatitis, allergies, etc. P1 is useful for treating or preventing
 CC type II diabetes mellitus, hyperglycemia, respiratory disorders
 CC including inhalation. P1 is useful in treating or preventing retinopathy,
 CC nephropathy and edema formation. P1 is useful for treating or preventing
 CC headache, anxiety, sleep disorders and memory loss. P1 is useful as a
 CC marker to identify, detect, stage, or diagnosis diseases and conditions
 CC of the small intestine, including Crohn's disease, colitis, inflammatory
 CC bowel disease, tumours, etc. P1 can be conjugated to diagnostic or
 CC therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
 CC fibrosis lesions and specific cells lining the intestinal tract, thus
 CC useful in targeting radioactive moieties or therapeutic moieties to the
 CC intestine to aid in imaging and diagnosing or treating
 CC colorectal/metastasised or local colorectal cancer. The current sequence
 CC represents a bacterial ST peptide which is an activator of the GC-C
 CC receptor. ST peptides are considered super agonists of GC-C and are very
 CC resistant to proteolytic degradation.

XX Sequence 18 AA;

Query Match 94.7%; Score 18; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 NTFYCCCLCCNPACAGCY 19

Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 15

ADR48341 94.7%; Score 18; DB 8; Length 18;
 ID ADR48341 standard; peptide; 18 AA.

XX AC ADR48341;

XX DT 04-NOV-2004 (first entry)

XX DE Bacterial ST peptide #2.

XX	Gastrointestinal; antiinflammatory; laxative; cardiac; antiulcer;
KW	anorectic; cardiovascular; cytosolic; analgesic; CNS; respiratory;
KW	neuroprotective; vasotropic; auditory; antiemetic; antisthmatic;
KW	nephrotropic; hepatotropic; virucide; immunosuppressive; antiallergic;
KW	antidiabetic; ophthalmological; tranquiliser; hypnotic; nootropic;
KW	guanylate cyclase C; GC-C; receptor; gastroesophageal disorder;
KW	irritable bowel syndrome; constipation; gastroesophageal reflux disease;
KW	heartburn; dyspepsia; gastroparesis; Crohn's disease; ulcerative colitis;
KW	inflammatory bowel disease; obesity; heart failure; cystic fibrosis;
KW	cancer; respiratory disorder; neurological disorder; carbonate imbalance;
KW	erectile dysfunction; inner ear disorder; slow digestion; nausea;
KW	vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy;
KW	retinopathy; nephropathy; headache; anxiety; sleep disorder.
XX	
OS	Escherichia coli.
XX	
PN	WO2004069165-A2.
PN	
PD	19-AUG-2004.
XX	
PF	28-JAN-2004; 2004WO-US002390.
XX	
PR	28-JAN-2003; 2003US-0443098P.
PR	15-MAY-2003; 2003US-0471289P.
PR	12-NOV-2003; 2003US-0519460P.
XX	
XX	(MICR-) MICROBIA INC.
PA	
XX	Currie MG, Mahajan-Miklos S;
XX	
XX	WPI; 2004-604332/58.
DR	
XX	
PT	Novel purified peptide capable of activating the guanylate cyclase C
PT	receptor, useful for treating obesity, congestive heart failure and
PT	benign prostatic hyperplasia.
XX	
XX	Disclosure; Page 29; 93pp; English.
XX	
CC	The invention relates to a purified peptide (P1) capable of activating
CC	the guanylate cyclase C (GC-C) receptor. Further disclosed is a
CC	pharmaceutical composition comprising the peptide of the invention. The
CC	composition of the invention is useful for treating a gastrointestinal
CC	disorder in a patient, which involves administering P1, where the
CC	gastrointestinal disorder is gastrointestinal motility disorder,
CC	irritable bowel syndrome, chronic constipation, a functional
CC	gastrointestinal disorder, gastroesophageal reflux disease, functional
CC	heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
CC	gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
CC	obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel
CC	disease. The peptide of the invention is also useful for treating
CC	obesity, congestive heart failure, cystic fibrosis or a patient suffering
CC	from constipation. The P1/GC-C receptor agonist is useful for treating
CC	cancer, respiratory disorder, neurological disorder, disorder associated
CC	with carbonate imbalance, erectile dysfunction, insulin-related disorder
CC	or inner ear disorder. P1 is useful in treating slow digestion or slow
CC	stomach emptying. P1 is useful in relieving symptoms of gastroparesis
CC	such as nausea, vomiting, bloating, and delayed gastric emptying. P1 is
CC	useful for treating or preventing asthma, nephritis, hepatitis,
CC	pancreatitis, allergies, etc. P1 is useful for treating or preventing
CC	type II diabetes mellitus, hyperglycaemia, respiratory disorders
CC	including inhalation. P1 is useful in treating or preventing retinopathy,
CC	nephropathy and edema formation. P1 is useful for treating or preventing
CC	headache, anxiety, sleep disorders and memory loss. P1 is useful as a
CC	marker to identify, detect, stage, or diagnosis diseases and conditions
CC	of the small intestine, including Crohn's disease, colitis, inflammatory
CC	bowel disease, tumours, etc. P1 can be conjugated to diagnostic or
CC	therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
CC	fibrosis lesions and specific cells lining the intestinal tract, thus
CC	useful in aiding radioactive moieties or therapeutic moieties to the
CC	intestine to aid in imaging and diagnosing or treating
CC	colorectal/metastasised or local colorectal cancer. The current sequence
CC	represents a bacterial ST peptide which is an activator of the GC-C

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CC receptor. ST peptides are considered super agonists of GC-C and are very
CC resistant to proteolytic degradation.
XX
SQ Sequence 18 AA;

Query Match          94.7%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      |||||
Db      1 NTFYCCELCNCPACAGCY 18

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GenCore version 5.1.6
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(without alignments)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	1	US-08-141-892A-2
2	19	100.0	19	2	US-08-583-447A-2
3	19	100.0	19	2	US-08-467-920-2
4	19	100.0	19	3	US-08-635-930-2
5	19	100.0	19	3	US-09-193-997-2
6	19	100.0	19	3	US-09-138-237A-2
7	18	94.7	18	1	US-08-141-892A-7
8	18	94.7	18	1	US-08-141-892A-13
9	18	94.7	18	1	US-08-141-892A-38
10	18	94.7	18	2	US-08-583-447A-7
11	18	94.7	18	2	US-08-583-447A-13
12	18	94.7	18	2	US-08-583-447A-38
13	18	94.7	18	2	US-08-467-920-7
14	18	94.7	18	2	US-08-467-920-13
15	18	94.7	18	2	US-08-467-920-38
16	18	94.7	18	3	US-08-635-930-7
17	18	94.7	18	3	US-08-635-930-13
18	18	94.7	18	3	US-08-635-930-38
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24	18	94.7	18	3	US-09-138-237A-38
25	17	89.5	17	1	US-08-141-892A-8
26	17	89.5	17	1	US-08-141-892A-14
27	17	89.5	17	1	US-08-141-892A-41

28	17	89.5	17	2	US-08-583-447A-8	Sequence 8, Appli
29	17	89.5	17	2	US-08-583-447A-14	Sequence 14, Appl
30	17	89.5	17	2	US-08-583-447A-41	Sequence 41, Appl
31	17	89.5	17	2	US-08-467-920-8	Sequence 8, Appli
32	17	89.5	17	2	US-08-467-920-14	Sequence 14, Appl
33	17	89.5	17	2	US-08-467-920-41	Sequence 41, Appl
34	17	89.5	17	3	US-08-635-930-8	Sequence 8, Appli
35	17	89.5	17	3	US-08-635-930-14	Sequence 14, Appl
36	17	89.5	17	3	US-08-635-930-41	Sequence 41, Appl
37	17	89.5	17	3	US-09-193-997-8	Sequence 8, Appli
38	17	89.5	17	3	US-09-193-997-14	Sequence 14, Appl
39	17	89.5	17	3	US-09-193-997-41	Sequence 41, Appl
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41	17	89.5	17	3	US-09-138-237A-14	Sequence 14, Appl
42	17	89.5	17	3	US-09-138-237A-41	Sequence 41, Appl
43	16	84.2	16	1	US-08-141-892A-9	Sequence 9, Appli
44	16	84.2	16	1	US-08-141-892A-15	Sequence 15, Appl
45	16	84.2	16	2	US-08-583-447A-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-141-892A-2
; Sequence 2, Application US/08141892A
; Patent No. 5518888
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
; TITLE OF INVENTION: of Using the Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 55188888ris
; STREET: One liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,892A
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0903
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-141-892A-2

Query Match 100.0%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8,9e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 NNTFYCCELCCNPACAGCY 19
Db 1 NNTFYCCELCCNPACAGCY 19

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-920-2
;
Query Match 100.0%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.9e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTFYCCCLCCNPACAGCY 19
Db 1 NNTFYCCCLCCNPACAGCY 19

RESULT 4
US-08-635-930-2
; Sequence 2, Application US/08635930
; Patent No. 6060037
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically Bind To
; TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using
; TITLE OF INVENTION: The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WordPerfect 6.0/6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,930
; FILING DATE: 26-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,056
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-583-447A-2
;
Query Match 100.0%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.9e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTFYCCCLCCNPACAGCY 19
Db 1 NNTFYCCCLCCNPACAGCY 19

RESULT 3
US-08-467-920-2
; Sequence 2, Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESS: No. 5962220ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103

```

REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1360
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-635-930-2

Query Match 100.0%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.9e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTFYCCELCNCPACGY 19
Db 1 NNTFYCCELCNCPACGY 19

RESULT 5

US-09-193-997-2
Sequence 2, Application US/09193997
Patent No. 6087109

GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically
Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 6087109ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,997

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,920
FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1589
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-193-997-2

Query Match 100.0%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.9e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTFYCCELCNCPACGY 19

Db 1 NNTFYCCELCNCPACGY 19

RESULT 6

US-09-138-237A-2
Sequence 2, Application US/09138237A
Patent No. 6268159

GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: Of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6268159ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,237A

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-138-237A-2

Query Match 100.0%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.9e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTFYCCELCNCPACGY 19
Db 1 NNTFYCCELCNCPACGY 19

RESULT 7

US-08-141-892A-7
Sequence 7, Application US/08141892A
Patent No. 5518888

GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: Of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:

Qy 1 NNTFYCCELCNCPACGY 19

; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,892A
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0903
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-141-892A-7

Query Match 94.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTFYCCCLCCNPACAGC 18
DB 1 NTFYCCCLCCNPACAGC 18

RESULT 8
US-08-141-892A-13
; Sequence 13, Application US/08141892A
; Patent No. 5518888
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
; TITLE OF INVENTION: of Using the Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,892A
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0903
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-141-892A-13

Query Match 94.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCCLCCNPACAGCY 19
DB 1 NTFYCCCLCCNPACAGCY 18

RESULT 9
US-08-141-892A-38
; Sequence 38, Application US/08141892A
; Patent No. 5518888
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
; TITLE OF INVENTION: of Using the Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,892A
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0903
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-141-892A-38

Query Match 94.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCCLCCNPACAGCY 19
DB 1 NTFYCCCLCCNPACAGCY 18

RESULT 10
US-08-583-447A-7
; Sequence 7, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and


```
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-583-447A-7

Query Match          94.7%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NNTFYCCELCCNPACAGC 18
Db 1 NNTFYCCELCCNPACAGC 18

RESULT 11
US-08-583-447A-13
; Sequence 13, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-583-447A-38

Query Match          94.7%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NNTFYCCELCCNPACAGC 18
Db 1 NNTFYCCELCCNPACAGC 18

RESULT 12
US-08-583-447A-38
; Sequence 38, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-583-447A-38

Query Match          94.7%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-583-447A-13

Query Match          94.7%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 NTFYCCELCCNPACAGCY 19
Db 1 NTFYCCELCCNPACAGCY 18

RESULT 12
US-08-583-447A-38
; Sequence 38, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-583-447A-38

Query Match          94.7%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 NTFYCCCLCCNPACAGCY 19
|||||
Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 13
US-08-467-920-7
; Sequence 7, Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; -ADDRESSEE: No. 5962220is
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-467-920-7

Query Match 94.7%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 14
US-08-467-920-13
; Sequence 13, Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

QY 1 NNTFYCCCLCCNPACAGC 18
|||||
Db 1 NNTFYCCCLCCNPACAGC 18

RESULT 14
US-08-467-920-13
; Sequence 13, Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

; ADDRESSEE: No. 5962220is
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-467-920-13

Query Match 94.7%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCCLCCNPACAGCY 19
|||||
Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 15
US-08-467-920-38
; Sequence 38, Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; -ADDRESSEE: No. 5962220is
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993

Search completed: March 26, 2005, 17:27:26
Job time : 25.7857 secs

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OM protein - protein search, using sw model

Run on: March 26, 2005, 17:25:02 ; Search time 61.4107 Seconds
(without alignments)
102.440 Million cell updates/sec

Title: US-10-775-481A-2

Perfect score: 19

Sequence: 1 NNTFYCELCCNPACAGCY 19

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1407402 seqs, 331100923 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	15	US-10-621-684-2
2	19	100.0	72	17	US-10-796-719-20
3	18	94.7	18	15	US-10-621-684-7
4	18	94.7	18	15	US-10-621-684-13
5	18	94.7	18	15	US-10-621-684-38
6	18	94.7	18	17	US-10-796-719-2
7	18	94.7	18	17	US-10-796-719-4
8	17	89.5	17	15	US-10-621-684-8
9	17	89.5	17	15	US-10-621-684-14
10	17	89.5	17	15	US-10-621-684-41
11	16	84.2	16	15	US-10-621-684-9
12	16	84.2	16	15	US-10-621-684-15
13	15	78.9	15	15	US-10-621-684-10
14	15	78.9	15	15	US-10-621-684-16
15	15	78.9	15	15	US-10-621-684-42
16	15	78.9	15	15	US-10-796-719-11
17	14	73.7	14	15	US-10-621-684-11
18	14	73.7	14	15	US-10-621-684-17
19	14	73.7	14	15	US-10-621-684-43
20	14	73.7	14	15	US-10-621-684-44
21	13	68.4	13	15	US-10-621-684-12
22	13	68.4	13	15	US-10-621-684-45
23	13	68.4	13	15	US-10-621-684-31
24	11	57.9	14	15	US-10-621-684-52
25	11	57.9	14	15	US-10-621-684-30
26	11	57.9	15	15	US-10-621-684-36
27	11	57.9	16	15	US-10-621-684-29
28	11	57.9	16	15	US-10-621-684-35
29	11	57.9	17	15	US-10-621-684-28
30	11	57.9	17	15	US-10-621-684-34
31	11	57.9	18	15	US-10-621-684-27
32	11	57.9	18	15	US-10-621-684-33
33	11	57.9	18	15	US-10-621-684-40
34	11	57.9	19	14	US-10-107-814-23
35	11	57.9	19	15	US-10-371-966-1
36	11	57.9	19	15	US-10-371-966-2
37	11	57.9	19	15	US-10-621-684-5
38	11	57.9	19	17	US-10-796-719-1
39	11	57.9	19	17	US-10-796-719-26
40	11	57.9	19	17	US-10-796-719-27
41	11	57.9	19	17	US-10-479-606-7
42	11	57.9	21	17	US-10-796-719-39
43	11	57.9	21	17	US-10-796-719-40
44	11	57.9	72	17	US-10-796-719-21
45	10	52.6	13	15	US-10-621-684-32

ALIGNMENTS

RESULT 1

US-10-621-684-2
; Sequence 2, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods of Using the Same

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1

STREET: One Liberty Place, 46th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows

SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/621.684

FILING DATE: 17-Jul-2003

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/583.447A

FILING DATE: 05-JAN-1996

APPLICATION NUMBER: US 08/141.892

FILING DATE: 26-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: DeLuca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-1702

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

```
;
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-621-684-2

Query Match 100.0%; Score 19; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNTFYCCCLCCNPACAGY 19
Db 1 NNTFYCCCLCCNPACAGY 19

RESULT 2
US-10-796-719-20
; Sequence 20, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; TYPE: PRT
; LENGTH: 72
; ORGANISM: Escherichia coli
US-10-796-719-20

Query Match 100.0%; Score 19; DB 17; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNTFYCCCLCCNPACAGY 19
Db 54 NNTFYCCCLCCNPACAGY 72

RESULT 3
US-10-621-684-7
; Sequence 7, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
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```
;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-621-684-7

Query Match 94.7%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.2e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNTFYCCCLCCNPACAGC 18
Db 1 NNTFYCCCLCCNPACAGC 18

RESULT 4
US-10-621-684-13
; Sequence 13, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
```

```
;
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-621-684-13

Query Match          94.7%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.2e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 NTFYCCCLCCNPACAGCY 19
Db      1 NTFYCCCLCCNPACAGCY 18

RESULT 5
US-10-621-684-38
; Sequence 38, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621.684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583.447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141.892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCCT NUMBER: T0U-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-621-684-38

Query Match          94.7%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.2e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 NTFYCCCLCCNPACAGCY 19
Db      1 NTFYCCCLCCNPACAGCY 18
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RESULT 6
US-10-796-719-2
; Sequence 2, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796.719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-796-719-2

Query Match          94.7%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.2e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 NTFYCCCLCCNPACAGCY 19
Db      1 NTFYCCCLCCNPACAGCY 18

RESULT 7
US-10-796-719-4
; Sequence 4, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796.719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Citrobacter freundlii
US-10-796-719-4

Query Match          94.7%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.2e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 NTFYCCCLCCNPACAGCY 19
Db      1 NTFYCCCLCCNPACAGCY 18
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Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 8

US-10-621-684-8

; Sequence 8, Application US/10621684

; Publication No. US20040029182A1

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.

; TITLE OF INVENTION: ST Receptor Binding Compounds and

; Methods of Using the Same

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris

; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/621,684

; FILING DATE: 17-Jul-2003

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/583,447A

; FILING DATE: 05-JAN-1996

; APPLICATION NUMBER: US 08/141,892

; FILING DATE: 26-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: TJU-1702

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-621-684-8

Query Match 89.5%; Score 17; DB 15; Length 17;

Best Local Similarity 100.0%; Pred. No. 8.4e-12;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCCLCCNPACAGC 18

Db 1 NTFYCCCLCCNPACAGC 17

RESULT 9

US-10-621-684-14

; Sequence 14, Application US/10621684

; Publication No. US20040029182A1

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.

; TITLE OF INVENTION: ST Receptor Binding Compounds and

; Methods of Using the Same

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris

; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/621,684

; FILING DATE: 17-Jul-2003

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/583,447A

; FILING DATE: 05-JAN-1996

; APPLICATION NUMBER: US 08/141,892

; FILING DATE: 26-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

US-10-621-684-14

Query Match 89.5%; Score 17; DB 15; Length 17;

Best Local Similarity 100.0%; Pred. No. 8.4e-12;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCCLCCNPACAGC 18

Db 1 NTFYCCCLCCNPACAGC 17

RESULT 9

US-10-621-684-14

; Sequence 14, Application US/10621684

; Publication No. US20040029182A1

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.

; TITLE OF INVENTION: ST Receptor Binding Compounds and

; Methods of Using the Same

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris

; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/621,684

; FILING DATE: 17-Jul-2003

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/583,447A

; FILING DATE: 05-JAN-1996

; APPLICATION NUMBER: US 08/141,892

; FILING DATE: 26-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

US-10-621-684-14

Query Match 89.5%; Score 17; DB 15; Length 17;

Best Local Similarity 100.0%; Pred. No. 8.4e-12;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCCLCCNPACAGC 18

Db 1 NTFYCCCLCCNPACAGC 17

RESULT 9

US-10-621-684-14

; Sequence 14, Application US/10621684

; Publication No. US20040029182A1

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.

; TITLE OF INVENTION: ST Receptor Binding Compounds and

; Methods of Using the Same

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris

; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/621,684

; FILING DATE: 17-Jul-2003

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/583,447A

; FILING DATE: 05-JAN-1996

; APPLICATION NUMBER: US 08/141,892

; FILING DATE: 26-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

US-10-621-684-14

Query Match 89.5%; Score 17; DB 15; Length 17;

Best Local Similarity 100.0%; Pred. No. 8.4e-12;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCCLCCNPACAGC 18

Db 1 NTFYCCCLCCNPACAGC 17

RESULT 9

US-10-621-684-14

; Sequence 14, Application US/10621684

; Publication No. US20040029182A1

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.

; TITLE OF INVENTION: ST Receptor Binding Compounds and

; Methods of Using the Same

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris

; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/621,684

; FILING DATE: 17-Jul-2003

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/583,447A

; FILING DATE: 05-JAN-1996

; APPLICATION NUMBER: US 08/141,892

; FILING DATE: 26-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

US-10-621-684-14

Query Match 89.5%; Score 17; DB 15; Length 17;

Best Local Similarity 100.0%; Pred. No. 8.4e-12;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCCLCCNPACAGC 18

Db 1 NTFYCCCLCCNPACAGC 17

RESULT 9

US-10-621-684-14

; Sequence 14, Application US/10621684

; Publication No. US20040029182A1

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.

; TITLE OF INVENTION: ST Receptor Binding Compounds and

; Methods of Using the Same

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris

; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/621,684

; FILING DATE: 17-Jul-2003

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/583,447A

; FILING DATE: 05-JAN-1996

; APPLICATION NUMBER: US 08/141,892

; FILING DATE: 26-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

US-10-621-684-14

Query Match 89.5%; Score 17; DB 15; Length 17;

Best Local Similarity 100.0%; Pred. No. 8.4e-12;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCCLCCNPACAGC 18

Db 1 NTFYCCCLCCNPACAGC 17

RESULT 9

US-10-621-684-14

; Sequence 14, Application US/10621684

; Publication No. US20040029182A1

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.

; TITLE OF INVENTION: ST Receptor Binding Compounds and

; Methods of Using the Same

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris

; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/621,684

; FILING DATE: 17-Jul-2003

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/583,447A

; FILING DATE: 05-JAN-1996

; APPLICATION NUMBER: US 08/141,892

; FILING DATE: 26-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-621-684-41

Query Match 89.5%; Score 17; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.4e-12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACGC 18

Db 1 NTFYCCCLCCNPACGC 17

RESULT 11

US-10-621-684-9
Sequence 9, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
Methods of Using the Same

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/621.684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/583.447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141.892
FILING DATE: 26-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: DeLuca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-1702

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-621-684-9

Query Match 84.2%; Score 16; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.9e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TFYCCCLCCNPACGC 18

Db 1 TFYCCCLCCNPACGC 16

RESULT 12

US-10-621-684-15
Sequence 15, Application US/10621684
Publication No. US20040029182A1

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: ST Receptor Binding Compounds and

Methods of Using the Same

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris

STREET: One Liberty Place, 46th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows

SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/621.684

FILING DATE: 17-Jul-2003

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/583.447A

FILING DATE: 05-JAN-1996

APPLICATION NUMBER: US 08/141.892

FILING DATE: 26-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: DeLuca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-1702

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-10-621-684-15

Query Match 84.2%; Score 16; DB 15; Length 16;

Best Local Similarity 100.0%; Pred. No. 9.9e-11;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FYCCCLCCNPACGCY 19

Db 1 FYCCCLCCNPACGCY 16

RESULT 13

US-10-621-684-10

Sequence 10, Application US/10621684

Publication No. US20040029182A1

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: ST Receptor Binding Compounds and

Methods of Using the Same

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris

STREET: One Liberty Place, 46th Floor

CITY: Philadelphia

STATE: Pennsylvania

Qy

/ COUNTRY: USA
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: Windows
/ SOFTWARE: WordPerfect 6.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/621,684
/ FILING DATE: 17-Jul-2003
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/583,447A
/ FILING DATE: 05-JAN-1996
/ APPLICATION NUMBER: US 08/141,892
/ FILING DATE: 26-OCT-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DeLuca, Mark
/ REFERENCE/DOCKET NUMBER: 33,229
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-568-3100
/ TELEFAX: 215-568-3439
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-621-684-10

Query Match 78.9%; Score 15; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYCCELCNCPACAGC 18
| | | | | | | | | | | | | | | | | |
Db 1 FYCCELCNCPACAGC 15

RESULT 14
US-10-621-684-16
; Sequence 16, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: Windows
/ SOFTWARE: WordPerfect 6.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/621,684
/ FILING DATE: 17-Jul-2003
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/583,447A
/ FILING DATE: 05-JAN-1996
/ APPLICATION NUMBER: US 08/141,892
/ FILING DATE: 26-OCT-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DeLuca, Mark

/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: TJU-1702
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-568-3100
/ TELEFAX: 215-568-3439
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-621-684-16

Query Match 78.9%; Score 15; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YCCELCNCPACAGCY 19
| | | | | | | | | | | | | | | | | |
Db 1 YCCELCNCPACAGCY 15

RESULT 15
US-10-621-684-42
; Sequence 42, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: Windows
/ SOFTWARE: WordPerfect 6.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/621,684
/ FILING DATE: 17-Jul-2003
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/583,447A
/ FILING DATE: 05-JAN-1996
/ APPLICATION NUMBER: US 08/141,892
/ FILING DATE: 26-OCT-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DeLuca, Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: TJU-1702
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-568-3100
/ TELEFAX: 215-568-3439
/ INFORMATION FOR SEQ ID NO: 42:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-621-684-42

Query Match 78.9%; Score 15; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YCCELCGNPACGCY 19
| | | | | | | | | | | | | | | | | | | | | |
Db 1 YCCELCGNPACGCY 15

Search completed: March 26, 2005, 17:44:30
Job time : 61.4107 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2005, 17:10:31 ; Search time 19.6786 Seconds
(without alignments)
92.899 Million cell updates/sec

Title: US-10-775-481A-2

Perfect score: 19

Sequence: 1 NNTFYCCELCNCPACGY 19

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	72	1 QHEC1	heat-stable entero
2	18	94.7	18	2 A50103	heat-stable entero
3	11	57.9	72	1 QHEC4	heat-stable entero
4	11	57.9	72	1 QHEC1B	heat-stable entero
5	10	52.6	18	1 QHEC2	heat-stable entero
6	10	52.6	53	2 S68705	heat-stable entero
7	9	47.4	66	2 S31652	enterotoxin - Vers
8	9	47.4	71	2 S25659	heat-stable entero
9	6	31.6	13	2 A28953	alpha-conotoxin SI
10	6	31.6	15	1 NTKNAG	alpha-conotoxin GI
11	6	31.6	17	2 A45334	heat-stable entero
12	6	31.6	19	2 A44379	alpha-conotoxin SI
13	6	31.6	65	2 S34671	heat-stable entero
14	6	31.6	78	1 QHVC1	heat-stable entero
15	6	31.6	90	2 D85845	probable lysis pro
16	6	31.6	620	2 H82761	sulfur deprivation
17	6	31.6	924	2 E71476	alanine-tRNA ligas
18	5	26.3	55	2 S14212	NADH2 dehydrogenas
19	5	26.3	75	2 H84631	hypothetical prote
20	5	26.3	108	2 AF1043	hypothetical prote
21	5	26.3	110	2 I74319	gene EHS-2 protein
22	5	26.3	111	2 B72476	hypothetical prote
23	5	26.3	116	2 S75378	hypothetical prote
24	5	26.3	124	2 C96762	hypothetical prote
25	5	26.3	129	2 A24255	chorion class A pr
26	5	26.3	132	2 A10543	probable secreted
27	5	26.3	133	2 T17300	hypothetical prote
28	5	26.3	135	2 S34815	nifU protein - Rh
29	5	26.3	139	1 Q28P87	gene 2.8 protein -

RESULT 1

QHEC1

heat-stable enterotoxin ST-I precursor - Escherichia coli

N/Alternate names: heat-stable enterotoxin estal

C/Species: Escherichia coli

C/Date: 31-Aug-1980 #sequence revision 31-Aug-1980 #text_change 09-Jul-2004

C/Accession: A01822; A30985; A36732; J0374; I51932

R/So, M.; McCarthy, B.J.

Proc. Natl. Acad. Sci. U.S.A. 77, 4011-4015, 1980

A/Title: Nucleotide sequence of the bacterial transposon Tn1681 encoding a heat-stable (S

A/Reference number: A01822; MUID:81054703; PMID:6254008

A/Accession: A01822

A/Molecule type: DNA

A/Residues: 1-72 <LAZ>

A/Cross-references: UNIPROT:P01559; GB:V00612; GB:V01831; NID:G43704; PIDN:CAA23883.1; P

R/Lazarus, C.; Seidah, N.G.; Chretien, M.; Lallier, R.; St-Pierre, S.

Can. J. Biochem. Cell Biol. 61, 287-292, 1983

A/Title: Primary structure determination of Escherichia coli heat-stable enterotoxin of

A/Reference number: A30985; MUID:83284515; PMID:6349752

A/Accession: A30985

A/Molecule type: protein

A/Residues: 55-72 <LAZ2>

A/Experimental source: strain F11

R/Dallas, W.S.

J. Bacteriol. 172, 5490-5493, 1990

A/Title: The heat-stable toxin I gene from Escherichia coli 18D.

A/Reference number: A36732; MUID:90368614; PMID:2203756

A/Accession: A36732

A/Molecule type: DNA

A/Residues: 1-72 <DAL>

A/Cross-references: GB:M58746; NID:g145860; PIDN:AAA62776.1; PID:g145861

A/Experimental source: strain 18D

R/Stiegitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.;

Plasmid 20, 42-53, 1988

A/Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escheri

A/Reference number: J0373; MUID:89202548; PMID:3071819

A/Accession: J0374

A/Molecule type: DNA

A/Residues: 1-72 <STI>

R/Sekizaki, T.; Akashi, H.; Terakado, N.

Am. J. Vet. Res. 46, 909-912, 1985

A/Title: Nucleotide sequences of the genes for Escherichia coli heat-stable enterotoxin

A/Reference number: I51932; MUID:85249571; PMID:2990268

A/Accession: I51932

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-69, 'p', '71-72 <RES>

A/Cross-references: GB:M25607; NID:g147877; PIDN:AAA24653.1; PID:g147878

C/Comment: Both heat-stable and heat-labile enterotoxins are produced by pathogenic stra

ular sizes.

C/Superfamily: heat-stable enterotoxin ST

C/Keywords: enterotoxin; heat-stable protein

heterodisulfide re
hypothetical prote
hypothetical prote
probable rRNA meth
BioY family protei
conserved hypotet
probable pentose-5
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
aquaporin homolog
protein ZC123.3 li
cob(I)alamin adeno

F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-54/Domain: propeptide #status predicted <PRO>
F;55-72/Product: heat-stable enterotoxin ST-I #status experimental <MAT>
F;59-64,60-68,63-71/Disulfide bonds: #status predicted

Query Match 100.0%; Score 19; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 28-15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTFYCCELCCNPACAGCY 19
|||||
Db 54 NNTFYCCELCCNPACAGCY 72
|||||

RESULT 2
A60103
heat-stable enterotoxin ST-Ia - Citrobacter freundii
C;Species: Citrobacter freundii
C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C;Accession: A60103
R;Guarino, A.; Giannella, R.; Thompson, M.R.
Infect. Immun. 57, 649-652, 1989
A;Title: Citrobacter freundii produces an 18-amino-acid heat-stable enterotoxin identical to enterotoxin ST-I
A;Reference number: A60103; MUID:89108617; PMID:2912902
A;Accession: A60103
A;Molecule type: protein
A;Residues: 1-18 <GUA>
A;Cross-references: UNIPROT:Q7M0U3
C;Superfamily: heat-stable enterotoxin ST

Query Match 94.7%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NNTFYCCELCCNPACAGCY 19
|||||
Db 1 NNTFYCCELCCNPACAGCY 18
|||||

RESULT 3
QHEC4
heat-stable enterotoxin STA4 precursor - Escherichia coli
C;Species: Escherichia coli
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: J03773; A35978
R;Stieglicz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.; Plasmid 20, 42-53, 1988
A;Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escherichia coli heat-stable enterotoxin STA4
A;Reference number: J03773; MUID:89202548; PMID:3071819
A;Accession: J03773
A;Molecule type: DNA
A;Residues: 1-72 <STI>
A;Cross-references: UNIPROT:P07965; GB:J03311; NID:gl47875; PIDN:AAA24652.1; PID:gl47876
R;Zhou, X.; Shen, L.P.; Chi, C.W.
Toxin 28, 453-456, 1990
A;Title: Isolation and nucleotide sequence determination of a gene encoding a heat-stable enterotoxin from Escherichia coli
A;Reference number: A35978; MUID:90273381; PMID:2190361
A;Accession: A35978
A;Molecule type: DNA
A;Residues: 1-72 <ZHO>
C;Genetics:
A;Gene: estA4
C;Superfamily: heat-stable enterotoxin ST
C;Keywords: enterotoxin; heat-stable protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-53/Domain: propeptide #status predicted <PRO>
F;54-72/Product: heat-stable enterotoxin #status predicted <MAT>
F;59-64,60-68,63-71/Disulfide bonds: #status predicted

Query Match 57.9%; Score 11; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YCCELCCNPAC 15
|||||
Db 58 YCCELCCNPAC 68
|||||

RESULT 4
QHEC1B
heat-stable enterotoxin ST-Ib precursor - Escherichia coli
N;Alternate names: heat-stable enterotoxin ST-A2
C;Species: Escherichia coli
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: JS0292; A33068; A33067; A30567
R;Moseley, S.L.; Hardy, J.W.; Hug, M.I.; Echeverria, P.; Falkow, S.
Infect. Immun. 39, 1167-1174, 1983
A;Title: Isolation and nucleotide determination of a gene encoding a heat-stable enterotoxin from Escherichia coli
A;Reference number: JS0292; MUID:83184648; PMID:6341230
A;Accession: JS0292
A;Molecule type: DNA
A;Residues: 1-72 <MOS>
A;Cross-references: UNIPROT:Q47185; UNIPROT:P07965; GB:M34916; NID:gl46407; PIDN:AAA2399
R;Dwarakanath, P.; Visweswariah, S.S.; Subrahmanyam, Y.V.B.K.; Shanthi, G.; Jagannatha, I.
Gene 81, 219-226, 1989
A;Title: Cloning and hyperexpression of a gene encoding the heat-stable toxin of Escherichia coli
A;Reference number: A33068; MUID:90034194; PMID:2680769
A;Accession: A33068
A;Molecule type: DNA
A;Residues: 1-18, 'A', 20-72 <DWA>
A;Cross-references: GB:M29255; NID:gl48029; PIDN:AAA24686.1; PID:gl48030
R;Note: the authors translated the codon AAG for residue 2 as Val and CTA for residue 34
R;Aimoto, S.; Takao, T.; Shimonishi, Y.; Hara, S.; Takeda, T.; Takeda, Y.; Miwatani, T.
Eur. J. Biochem. 129, 257-263, 1982
A;Title: Amino acid sequence of heat-stable enterotoxin produced by human enterotoxigenic Escherichia coli
A;Reference number: A33067; MUID:83105138; PMID:6759126
A;Accession: A33067
A;Molecule type: protein
A;Residues: 54-72 <AIM>
R;Guzman-Verduzco, L.M.; Kupersztosz, Y.M.
Infect. Immun. 57, 645-648, 1989
A;Title: Rectification of two Escherichia coli heat-stable enterotoxin allele sequences
A;Reference number: A30567; MUID:89108616; PMID:2643580
A;Accession: A30567
A;Molecule type: DNA
A;Residues: 1-18, 'A', 20-24, 'AG', 27-41, 'V', 43-44, 'N', 46, 'E', 48, 'S', 50-72 <GUZ>
A;Cross-references: GB:M18345; NID:gl45862; PIDN:AAA23729.1; PID:gl45863
C;Comment: This is one of the type I heat-stable enterotoxins that are methanol-soluble.
C;Genetics:
A;Gene: st
C;Superfamily: heat-stable enterotoxin ST
C;Keywords: enterotoxin; heat-stable protein
F;1-53/Domain: signal sequence and propeptide #status predicted <SIG>
F;54-72/Product: heat-stable enterotoxin ST-Ib #status experimental <MAT>
F;59-64,60-68,63-71/Disulfide bonds: #status experimental

Query Match 57.9%; Score 11; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YCCELCCNPAC 15
|||||
Db 58 YCCELCCNPAC 68
|||||

RESULT 5
QHEC2
heat-stable enterotoxin ST-2 - Escherichia coli
C;Species: Escherichia coli
C;Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 09-Jul-2004
C;Accession: A01823
R;Chan, S.K.; Giannella, R.A.
J. Biol. Chem. 256, 7744-7746, 1981
A;Title: Amino acid sequence of heat-stable enterotoxin produced by Escherichia coli pathogenic for man
A;Reference number: A01823; MUID:81264141; PMID:7021541
A;Accession: A01823

A:Molecule type: protein
A:Residues: 1-18 <CHA>
A:Cross-references: UNIPROT:P01560
A:Experimental source: strain 18D, serotype 0.42:k86:H37
C:Comment: This enterotoxin is one of several, of differing molecular sizes, produced by isolates of the heat-stable enterotoxin ST-1.
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:1-18/Product: heat-stable enterotoxin ST-2 #status experimental <MAT>
F:5-10,6-14,9-17/Disulfide bonds: #status predicted

Query Match 52.6%; Score 10; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NTFYCCELC 11
Db 1 NTFYCCELC 10
|||||

RESULT 6
S68705
heat-stable enterotoxin Y-STc - Yersinia enterocolitica
C:Species: Yersinia enterocolitica
C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C:Accession: S68705
R:Yoshino, K.; Takao, T.; Huang, X.; Murata, H.; Nakao, H.; Takeda, T.; Shimonishi, Y.
FEBS Lett. 362, 319-322, 1995
A:Title: Characterization of a highly toxic, large molecular size heat-stable enterotoxin
A:Reference number: S68705; MUID:95246844; PMID:7729521
A:Accession: S68705
A:Molecule type: protein
A:Residues: 1-53 <YOS>
A:Experimental source: strain 86-11
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:41-46,42-50,45-53/Disulfide bonds: #status predicted

Query Match 52.6%; Score 10; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 5.3e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCELCNCPAC 15
Db 41 CCELCNCPAC 50
|||||

RESULT 7
S31652
enterotoxin - Yersinia kristensenii
C:Species: Yersinia kristensenii
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S31652
R:Abraham, A.; Liesack, W.; Stackebrandt, E.
submitted to the EMBL Data Library, November 1992
A:Reference number: S31652
A:Accession: S31652
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-66 <IBR>
A:Cross-references: UNIPROT:P31518; EMBL:X69218; NID:G48617; PIDN:CAA49152.1; PID:G48618
C:Superfamily: heat-stable enterotoxin ST

Query Match 47.4%; Score 9; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CCNPACAGC 18
Db 58 CCNPACAGC 66
|||||

RESULT 8
A28953
alpha-conotoxin SI - cone shell (Conus striatus)
C:Species: Conus striatus (striated cone)
C:Date: 30-Jun-1989 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: A28953
R:Zafaralla, G.C.; Ramilo, C.; Gray, W.R.; Karlstrom, R.; Olivera, B.M.; Cruz, L.J.
Biochemistry 27, 7102-7105, 1988
A:Title: Phylogenetic specificity of cholinergic ligands: alpha-conotoxin SI.
A:Reference number: A28953; MUID:89062448; PMID:3196703
A:Accession: A28953
A:Molecule type: protein
A:Residues: 1-13 <ZAP>
A:Cross-references: UNIPROT:P15471
A:Note: this sequence was confirmed by chemical synthesis
C:Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholinesterase
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurotoxin

S25659
heat-stable enterotoxin yst precursor - Yersinia enterocolitica
C:Species: Yersinia enterocolitica
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S25659; A41474; A23114; S65849
R:Abraham, A.; Liesack, W.; Pike, S.; Stackebrandt, E.
FEBS Microbiol. Lett. 97, 63-66, 1992
A:Title: The polymerase chain reaction: an epidemiological tool to differentiate between Yersinia enterocolitica strains
A:Reference number: S25659
A:Accession: S25659
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-71 <IBR>
A:Cross-references: UNIPROT:P07593; EMBL:X65999; NID:G48611; PIDN:CAA46801.1; PID:G48612
R:Delor, I.; Kaeckenbeeck, A.; Wauters, G.; Cornelis, G.R.
Infect. Immun. 58, 2983-2988, 1990
A:Title: Nucleotide sequence of yst, the Yersinia enterocolitica gene encoding the heat-stable enterotoxin
A:Reference number: A41474; MUID:90354067; PMID:2201642
A:Accession: A41474
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-47, 'S', 49-71
A:Cross-references: GB:U09235; NID:G487394; PIDN:AAA18472.1; PID:G487395
R:Takao, T.; Tomimaga, N.; Yoshimura, S.; Shimonishi, Y.; Hara, S.; Inoue, T.; Miyama, A.
Eur. J. Biochem. 152, 199-206, 1985
A:Title: Isolation, primary structure and synthesis of heat-stable enterotoxin produced by Yersinia enterocolitica
A:Reference number: A23114; MUID:86004705; PMID:4043080
A:Accession: A23114
A:Molecule type: protein
A:Residues: 54-71 <AK>
R:Mikulskis, A.V.; Delor, I.; Ha Thi, V.; Cornelis, G.R.
Mol. Microbiol. 14, 905-915, 1994
A:Title: Regulation of the Yersinia enterocolitica enterotoxin yst gene. Influence of growth conditions
A:Reference number: S65849; MUID:95231297; PMID:7715452
A:Accession: S65849
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-43 <MIK>
A:Cross-references: EMBL:U09235
C:Genetics:
A:Gene: yst
C:Superfamily: heat-stable enterotoxin ST
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-41/Domain: propeptide #status predicted <PRO>
F:42-71/Product: heat-stable enterotoxin yst #status predicted <MAT>

Query Match 47.4%; Score 9; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.00095;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CCNPACAGC 18
Db 63 CCNPACAGC 71
|||||

RESULT 9
A28953
alpha-conotoxin SI - cone shell (Conus striatus)
C:Species: Conus striatus (striated cone)
C:Date: 30-Jun-1989 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: A28953
R:Zafaralla, G.C.; Ramilo, C.; Gray, W.R.; Karlstrom, R.; Olivera, B.M.; Cruz, L.J.
Biochemistry 27, 7102-7105, 1988
A:Title: Phylogenetic specificity of cholinergic ligands: alpha-conotoxin SI.
A:Reference number: A28953; MUID:89062448; PMID:3196703
A:Accession: A28953
A:Molecule type: protein
A:Residues: 1-13 <ZAP>
A:Cross-references: UNIPROT:P15471
A:Note: this sequence was confirmed by chemical synthesis
C:Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholinesterase
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurotoxin

F;2-7,3-13/Disulfide bonds: #status experimental
F;13/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 31.6%; Score 6; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCNPAC 15
Db 2 CCNPAC 7

RESULT 10

NTKNAG

alpha-conotoxin GIA [validated] - cone shell (Conus geographus)

N/Alternate names: alpha-Crx-GIA

N/Contains: alpha-conotoxin GI

C/Species: Conus geographus (geography cone)

C/Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 09-Jul-2004

C/Accession: A01782

R/Gray, W.R.; Luque, A.; Olivera, B.M.; Barrett, J.; Cruz, L.J.

J. Biol. Chem. 256, 4734-4740, 1981

A/Title: Peptide toxins from Conus geographus venom.

A/Reference number: A92320; MUID:81191854; PMID:7014556

A/Accession: A01782

A/Molecule type: protein

A/Residues: 1-15 <GRA>

A/Cross-references: UNIPROT:P01519

R/Gray, W.R.; Rivier, J.E.; Galyean, R.; Cruz, L.J.; Olivera, B.M.

J. Biol. Chem. 258, 12247-12251, 1983

A/Title: Conotoxin M1. Disulfide bonding and conformational states.

A/Reference number: A92396; MUID:84032400; PMID:6630187

A/Contents: annotation; disulfide bonds

R/Guddat, L.W.; Shan, L.; Martin, J.L.; Edmundson, A.B.; Gray, W.R.

submitted to the Brookhaven Protein Data Bank, May 1996

A/Reference number: A66253; PDB:1NOT

A/Contents: annotation; X-ray crystallography, 1.2 angstroms, residues 1-13

R/Guddat, L.W.; Martin, J.A.; Shan, L.; Edmundson, A.B.; Gray, W.R.

Biochemistry 35, 11329-11335, 1996

A/Title: Three-dimensional structure of the alpha-conotoxin GI at 1.2 angstroms resolution

A/Reference number: A58592; MUID:96378624; PMID:8784187

A/Contents: annotation; X-ray crystallography, 1.2 angstroms

R/Fardi, A.; Galdes, A.; Florance, J.; Maniconte, D.

Biochemistry 28, 5494-5501, 1989

A/Title: Solution structures of alpha-conotoxin GI determined by two-dimensional NMR spectroscopy

A/Reference number: A30629; MUID:89375269; PMID:2775719

A/Contents: annotation; conformation by (1)H-NMR

C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic

C/Superfamily: alpha-conotoxin

C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; blocked carboxyl end

F;1-13/Product: conotoxin GI #status experimental <GIA>

F;2-7,3-13/Disulfide bonds: #link GIA #status predicted

F;2-7,3-13/Disulfide bonds: #link GIA #status experimental

F;13/Modified site: amidated carboxyl end (Cys) (amide in mature form from following gly

F;15/Modified site: blocked carboxyl end (Lys) (probably amidated) #status experimental

Query Match 31.6%; Score 6; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCNPAC 15
Db 2 CCNPAC 7

RESULT 11

A54534

heat-stable enterotoxin - Vibrio mimicus (fragment)

C/Species: Vibrio mimicus

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-May-1996

C/Accession: A54534

R/Arita, M.; Honda, T.; Miwatani, T.; Takeda, T.; Takao, T.; Shimonishi, Y.

FEBS Microbiol. Lett. 79, 105-110, 1991

A/Title: Purification and characterization of a heat-stable enterotoxin of Vibrio mimicus
A/Reference number: A54534

A/Accession: A54534

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-17 <ARI>

C/Superfamily: heat-stable enterotoxin ST

Query Match 31.6%; Score 6; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCNPAC 15
Db 7 CCNPAC 12

RESULT 12

A44379

alpha-conotoxin SII - cone shell (Conus striatus)

C/Species: Conus striatus (striated cone)

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999

C/Accession: A44379

R/Ramilo, C.A.; Zafaralla, G.C.; Nadasdi, L.; Hammerland, L.G.; Yoshikami, D.; Gray, W.R.

Biochemistry 31, 9919-9926, 1992

A/Title: Novel alpha- and omega-conotoxins from Conus striatus venom.

A/Reference number: A44379; MUID:93003172; PMID:1390774

A/Accession: A44379

A/Molecule type: protein

A/Residues: 1-19 <RAM>

A/Cross-references: CAS:143294-31-9; PIDN:AB23762.1; PID:9257934

A/Experimental source: venom

A/Note: sequence extracted from NCBI backbone (NCBIP:116000); structure confirmed by chen

C/Comment: This peptide is an acetylcholine receptor blocker.

C/Superfamily: alpha-conotoxin

C/Keywords: acetylcholine receptor inhibitor; postsynaptic neurotoxin; venom

F;2-18,3-8,4-14/Disulfide bonds: #status predicted

F;19/Modified site: amidated carboxyl end (Ser) #status absent

Query Match 31.6%; Score 6; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCNPAC 15
Db 3 CCNPAC 8

RESULT 13

S34671

heat-stable enterotoxin - Vibrio cholerae (fragment)

C/Species: Vibrio cholerae

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S34671

R/Rosolini, G.M.; Lombardi, G.; Guglielmetti, P.

submitted to the EMBL Data Library, July 1993

A/Description: Detection of the Vibrio cholerae heat-stable enterotoxin gene by polymerase

A/Reference number: S34671

A/Accession: S34671

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-65 <ROS>

A/Cross-references: UNIPROT:Q56643; EMBL:X74108

C/Superfamily: heat-stable enterotoxin ST

Query Match 31.6%; Score 6; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCNPAC 15
Db 59 CCNPAC 64

RESULT 14

QHVCI
heat-stable enterotoxin ST precursor - Vibrio cholerae
C:Species: Vibrio cholerae
C:Date: 17-Mar-1987 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
C:Accession: A1469; A01824; S34464; S34466; S34465; S34463
R:Ogawa, A.; Kato, J.I.; Watanabe, H.; Nair, B.G.; Takeda, T.
Infect. Immun. 58, 3325-3329, 1990
A:Title: Cloning and nucleotide sequence of a heat-stable enterotoxin gene from Vibrio cholerae
A:Reference number: A1469; MUID:90382953; PMID:2205577
A:Accession: A1469
A:Molecule type: DNA
A:Residues: 1-78 <OGA>
A:Cross-references: UNIPROT:P04429; GB:M85198; NID:g155237; PIDN:AAA64889.1;
R:Takao, T.; Shimonishi, Y.; Kobayashi, M.; Nishimura, O.; Arita, M.; Takeda, T.; Honda,
PBBS Lett. 193, 250-254, 1985
A:Title: Amino acid sequence of heat-stable enterotoxin produced by Vibrio cholerae non-
A:Reference number: A01824; MUID:86056320; PMID:4065341
A:Accession: A01824
A:Molecule type: protein
A:Residues: 62-78 <TAK>
A:Experimental source: non-O.1 aerovar
R:Yoshino, K.; Miyachi, M.; Takao, T.; Bag, P.K.; Xiaozhe, H.; Nair, G.B.; Takeda, T.; S
PBBS Lett. 326, 83-86, 1993
A:Title: Purification and sequence determination of heat-stable enterotoxin elaborated b
A:Reference number: S34463; MUID:93314823; PMID:8325391
A:Accession: S34464
A>Status: preliminary
A:Molecule type: protein
A:Residues: 61-78 <Y03>
A:Accession: S34466
A>Status: preliminary
A:Molecule type: protein
A:Residues: 51-78 <Y05>
A:Accession: S34465
A>Status: preliminary
A:Molecule type: protein
A:Residues: 60-78 <Y02>
A:Accession: S34463
A>Status: preliminary
A:Molecule type: protein
A:Residues: 62-78 <Y04>
C:Superfamily: enterotoxin; heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable enterotoxin
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-61/Domain: propeptide #status predicted <PRO>
F:62-78/Product: heat-stable enterotoxin ST #status experimental <MAT>
F:64-69,65-73,68-76/Disulfide bonds: #status predicted

Query Match 31.6%; Score 6; DB 1; Length 78;
Best Local Similarity 100.0%; Pred.No.3.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CCNPAC 15
Db 68 CCNPAC 73

RESULT 15

D85845
probable lysin protein S of prophage CP-933V Z3340 [imported] - Escherichia coli (strain
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence revision 16-Feb-2001 #text change 09-Jul-2004
C:Accession: D85845
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamou, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85845
A>Status: preliminary

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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:51:20 ; Search time 74.9821 Seconds
(without alignments)
129.758 Million cell updates/sec

Title: US-10-775-481A-2

Perfect score: 19

Sequence: 1 NNTFYCCELCNCPACAGCY 19

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	72	1 HST1_ECOLI	P01559 escherichia
2	18	94.7	18	2 Q7M0U3	Q7M0U3 citrobacter
3	16	84.2	61	2 Q6VEG9	Q6VEG9 escherichia
4	11	57.9	61	2 Q6VEG7	Q6VEG7 escherichia
5	11	57.9	61	2 Q6VEG8	Q6VEG8 escherichia
6	11	57.9	72	1 HST2_ECOLI	Q47185 escherichia
7	11	57.9	72	1 HST3_ECOLI	P07965 escherichia
8	10	52.6	18	1 HSTB_ECOLI	P01560 escherichia
9	10	52.6	72	1 HSTC_YEREN	O50319 yersinia en
10	9	47.4	66	1 HST_YERKR	P1518 yersinia kr
11	9	47.4	71	1 HSTB_YEREN	P07593 yersinia en
12	9	47.4	71	1 HSTB_YEREN	P74977 yersinia en
13	6	31.6	15	1 CXAA_CONGE	P01519 conus geogr
14	6	31.6	17	2 Q9S581	Q9S581 vibrio chol
15	6	31.6	18	2 Q9S580	Q9S580 vibrio chol
16	6	31.6	19	2 Q9S579	Q9S579 vibrio chol
17	6	31.6	28	2 Q9S578	Q9S578 vibrio chol
18	6	31.6	64	1 CXAI_CONST	P15471 conus stria
19	6	31.6	66	2 Q56643	Q56643 vibrio chol
20	6	31.6	72	1 CXA2_CONST	P28879 conus stria
21	6	31.6	78	1 HSTN_VIBCH	P04429 vibrio chol
22	6	31.6	78	1 HSTO_VIBCH	Q07425 vibrio chol
23	6	31.6	78	2 Q93G01	Q93G01 vibrio mimi
24	6	31.6	90	2 Q8X4M8	Q8X4M8 escherichia
25	6	31.6	96	2 Q7Y222	Q7Y222 stx1 conver
26	6	31.6	96	2 Q9T1L3	Q9T1L3 bacterioph
27	6	31.6	120	2 Q858Z4	Q858Z4 bacterioph
28	6	31.6	158	2 Q8SC52	Q8SC52 stx2 conver
29	6	31.6	276	2 Q96H89	Q96H89 homo sapien
30	6	31.6	415	2 Q8CZV0	Q8CZV0 yersinia pe
31	6	31.6	556	2 Q8VUI3	Q8VUI3 desulfovibr

32 6 31.6 619 2 Q9GNI9 Q9gni9-caenorhabdi
33 6 31.6 620 2 Q87AF0 Q87af0 xyella fas
34 6 31.6 620 2 Q9PF93 Q9pf93 xyella fas
35 6 31.6 645 2 Q8A2H6 Q8a2h6 bacteroides
36 6 31.6 3401 2 Q8IBQ3 Q8ibq3 plasmodium
37 5 26.3 15 1 GUAN_DIDMA P55936 didelphis m
38 5 26.3 40 1 CXAC_CONGE Q8erb2 conus geogr
39 5 26.3 45 2 Q83AK0 Q83ak0 coxiella bu
40 5 26.3 50 2 Q83BF3 Q83bf3 coxiella bu
41 5 26.3 57 2 Q83A72 Q83a72 coxiella bu
42 5 26.3 63 2 Q9STC3 Q9stc3 elaeis guin
43 5 26.3 65 2 Q62MM8 Q62mm8 burkholderi
44 5 26.3 66 2 Q6C751 Q6c751 yarrowia li
45 5 26.3 66 2 Q688G0 Q688g0 oryza sativ

ALIGNMENTS

RESULT 1
ID_HST1_ECOLI STANDARD; PRT; 72 AA.
AC P01559; Q47653;
DT 21-JUN-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Heat-stable enterotoxin ST-1A/ST-P precursor.
GN Name=stai;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSFOSON=Tn1681;
RX MEDLINE=81054703; PubMed=6254008;
RA So M., McCarthy B.J.;
RT "Nucleotide sequence of the bacterial transposon Tn1681 encoding a heat-stable (ST) toxin and its identification in enterotoxigenic Escherichia coli strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4011-4015(1980).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O42:K86:H37 / 18D / ETEC;
RX MEDLINE=90368614; PubMed=2203756;
RA Dallas W.S.;
RT "The heat-stable toxin I gene from Escherichia coli 18D.";
RL J. Bacteriol. 172:5490-5493(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=85249571; PubMed=2990268;
RA Sekizaki T., Akashi H., Terakado N.;
RT "Nucleotide sequences of the genes for Escherichia coli heat-stable enterotoxin I of bovine, avian, and porcine origins.";
RL Am. J. Vet. Res. 46:909-912(1985).
RN [4]
RP DISULFIDE BONDS
RX MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5;
RA Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T.,
RX Miwatani T., Takeda Y.;
RT "Mode of disulfide bond formation of a heat-stable enterotoxin (STh) produced by a human strain of enterotoxigenic Escherichia coli.";
RL FEBS Lett. 215:165-170(1987).
RN [5]
RP PROCESSING
RX MEDLINE=90368584; PubMed=2203746;
RA Okamoto K., Takahara M.;
RT "Synthesis of Escherichia coli heat-stable enterotoxin STp as a pre-pro form and role of the pro sequence in secretion.";
RL J. Bacteriol. 172:5260-5265(1990).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (0.89 ANGSTROMS) OF 59-71.
RX MEDLINE=94312375; PubMed=8038153;

RA Sato T., Ozaki H., Kitagawa Y., Katsube Y., Shimonishi Y.;
RT "Structural characteristics for biological activity of heat-stable
RT enterotoxin produced by enterotoxigenic Escherichia coli: X-ray
RT crystallography of weakly toxic and nontoxic analogs.";
RL Biochemistry 33:18641-18650(1994).
CC -1- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.
CC -----
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CC -----
DR EMBL; V00612; CAA23883.1; -;
DR EMBL; M58746; AAA62776.1; -;
DR EMBL; M25607; AAA24653.1; -;
DR PIR; A01822; QHEC1.
DR PDB; 1ETL; X-ray; @=59-71.
DR PDB; 1ETW; X-ray; @=-.
DR PDB; 1ETV; X-ray; @=-.
DR InterPro: IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW 3D-structure; Enterotoxin; Signal; Toxin; Transposable element.
FT SIGNAL 1 19
FT PROPEP 20 54
FT PEPTIDE 55 72 Heat-stable enterotoxin ST-IA/ST-P.
FT DISULFID 59 64
FT DISULFID 60 68
FT DISULFID 63 71
FT CONFLICT 70 70 G -> P (in Ref. 3).
FT TURN 61 62
FT TURN 65 67
FT TURN 69 70
SQ SEQUENCE 72 AA; 8075 MW; 9288B766B3988264 CRC64;
Query Match 100.0%; Score 19; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 8.8e-15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNTFYCCELCNCPACAGCY 19
Db 54 NNTFYCCELCNCPACAGCY 72

RESULT 2
ID Q7M0U3 PRELIMINARY; PRT; 18 AA.
AC Q7M0U3;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Heat-stable enterotoxin ST-1a.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP MEDLINE=89108617; PubMed=2912902;
RX Guarino A., Giannella R., Thompson M.R.;
RA "Citrobacter freundii produces an 18-amino-acid heat-stable
RT enterotoxin identical to the 18-amino-acid Escherichia coli heat-
RT stable enterotoxin (ST 1a).";
RL Infect. Immun. 57:649-652(1989).
DR PIR; A60103;
DR HSSP; P01559; 1ETN.

DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
SQ SEQUENCE 18 AA; 1978 MW; D4D975F49D60064F CRC64;

Query Match 94.7%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e-14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NNTFYCCELCNCPACAGCY 19
Db 1 NNTFYCCELCNCPACAGCY 18

RESULT 3
Q6VEG9
ID Q6VEG9 PRELIMINARY; PRT; 61 AA.
AC Q6VEG9;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Heat-stable enterotoxin ST-1a (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F7682;
RX PubMed=15364995;
RA Reischl U., Youssef M.T., Wolf H., Hyttia-Trees E., Strockbine N.A.;
RT "Real-time fluorescence PCR assays for detection and characterization
RT of heat-labile I and heat-stable I enterotoxin genes from
RT enterotoxigenic Escherichia coli.";
RL J. Clin. Microbiol. 42:4092-4100(2004).
DR EMBL; AY342057; AAQ92974.1; -;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
FT NON_TER 1 1
SQ SEQUENCE 61 AA; 6927 MW; 646D4AE2F899D957 CRC64;

Query Match 84.2%; Score 16; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNTFYCCELCNCPACA 16
Db 43 NNTFYCCELCNCPACA 58

RESULT 4
Q6VEG7
ID Q6VEG7 PRELIMINARY; PRT; 61 AA.
AC Q6VEG7;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Heat-stable enterotoxin ST 1b (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E544;
RX PubMed=15364995;
RA Reischl U., Youssef M.T., Wolf H., Hyttia-Trees E., Strockbine N.A.;
RT "Real-time fluorescence PCR assays for detection and characterization
RT of heat-labile I and heat-stable I enterotoxin genes from

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SEQUENCE FROM N.A.
RX MEDLINE=89108616; PubMed=2643580;
RA Guzman-Verduzio L.M., Kuperstoch Y.M.;
RT "Rectification of two Escherichia coli heat-stable enterotoxin allele
RT sequences and lack of biological effect of changing the carboxy-
RT terminal tyrosine to histidine.";
RL Infect. Immun. 57:645-648(1989).
CC -!- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
-----
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-----
EMBL: M18345; AAA23729.1; --
PIR: JS0292; QHECIB.
HSP: P01559; LETN.
InterPro: IPR001489; Enterotoxin HS.
Pfam: PF02048; Enterotoxin HS; 1.
PROSITE: PS00273; ENTEROTOXIN_H_STABLE; 1.
Enterotoxin; Signal; Toxin.
SIGNAL 1 19 Potential.
FT PROPEP 20 53 By similarity.
FT PEPTIDE 54 72 Heat-stable enterotoxin A2.
FT DISULFID 59 64 By similarity.
FT DISULFID 60 68 By similarity.
FT DISULFID 63 71 By similarity.
FT DISULFID 63 71 By similarity.
FT SEQUENCE 72 AA; 7895 MW; D8785030E06B260 CRC64;

Query Match 57.9%; Score 11; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YCELCCHNPAC 15
|||||
DB 58 YCELCCHNPAC 68

RESULT 7
HST3_ECOLI STANDARD; PRT; 72 AA.
ID HST3_ECOLI AC P07965; P26588;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin A3/A4 precursor (STA3/STA4) (ST-H).
GN Name=sta3; Synonyms=sta4;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RN [1]
SEQUENCE FROM N.A.
RP RP STRAIN=153837-2;
RX MEDLINE=89202548; PubMed=3071819;
RA Stieglitz H., Cervantes L., Robledo R., Fonseca R., Covarrubias L.,
RA Bolivar F., Kuperstoch Y.M.;
RA "Cloning, sequencing, and expression in Ficol-generated minicells of
RT an Escherichia coli heat-stable enterotoxin gene.";
RL Plasmid 20:42-53(1988).
RN [2]
SEQUENCE FROM N.A.
RP RP STRAIN=153837-2;
RC MEDLINE=83184648; PubMed=6341230;
RX Moseley S.B., Hardy J.W., Huq M.I., Echeverria P., Falkow S.;
RA "Isolation and nucleotide sequence determination of a gene encoding a
RT heat-stable enterotoxin of Escherichia coli.";
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FT	PROPEP	20	53
FT	PEPTIDE	54	72
FT	DISULFID	59	64
FT	DISULFID	60	68
FT	DISULFID	63	71
FT	CONFLICT	19	19
SQ	SEQUENCE	72 AA; 7909 MW;	A -> P (in Ref. 2). 1CS9292BFCBA6BA CRC64;
Query Match			
Best Local Similarity 57.9%; Score 11; DB 1; Length 72;			
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Oy	5 YCCELCNPPAC 15		
Db	58 YCCELCNPPAC 68		
RESULT 8			
ID	HSTB_ECOLI	STANDARD;	PRT; 18 AA.
AC	P01560;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, last sequence update)		
DT	05-JUL-2004 (Rel. 44, last annotation update)		
DE	Heat-stable enterotoxin ST-2 (ST-B).		
OS	Escherichia coli.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		
OC	Enterobacteriaceae; Escherichia.		
OK	NCBI_TaxID=562;		
RN	[1]		
RP	SEQUENCE.		
RC	STRAIN=O42:K86:H37 / 18D / ETEC;		
RX	MEDLINE=81264141; PubMed=7021541;		
RA	Chan S.-K., Giannella R.A.;		
RA	Miwatani T., Takeda Y.;		
RT	"Amino acid sequence of heat-stable enterotoxin produced by		
RT	Escherichia coli pathogenic for man.";		
RL	J. Biol. Chem. 256:7744-7746(1981).		
CC	[2]		
RP	DISULFIDE BONDS		
RX	MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5;		
RA	Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T.,		
RA	Miwatani T., Takeda Y.;		
RT	"Mode of disulfide bond formation of a heat-stable enterotoxin (Sth)		
RT	produced by a human strain of enterotoxigenic Escherichia coli.";		
RL	FEB8 Lett 215:165-170(1987).		
CC	-1- FUNCTION: toxin which activates the particulate form of guanylate		
CC	cyclase and increases cyclic GMP levels within the host intestinal		
CC	epithelial cells.		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- SIMILARITY: Belongs to the heat-stable enterotoxin family.		
DR	PIR; A01823; QHEC2.		
DR	HSP; P01559; IETN.		
DR	InterPro; IPR001489; Enterotoxin HS.		
DR	Pfam; PF02048; Enterotoxin HS; 1.		
DR	PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.		
KW	Direct protein sequencing; Enterotoxin; Toxin.		
FT	DISULFID	5 10	
FT	DISULFID	6 14	
FT	DISULFID	9 17	
SQ	SEQUENCE	18 AA; 1978 MW;	DQC975F49D600650 CRC64;
Query Match			
Best Local Similarity 52.6%; Score 10; DB 1; Length 18;			
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Oy	2 NTFYCCELCC 11		
Db	1 NTFYCCELCC 10		
RESULT 9			
ID	HSTC_YEREN	STANDARD;	PRT; 72 AA.

AC 050319;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat-stable enterotoxin C precursor (V-57C).
 GN Name=yatC;
 OS Versinia enterocolitica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=630;
 RN (1) SEQUENCE FROM N.A.
 RP STRAIN=86-11;
 RC STRAIN=97202479; PubMed=9049998; DOI=10.1006/mpat.1996.0094;
 RX MEDLINE=97202479; PubMed=9049998; DOI=10.1006/mpat.1996.0094;
 RA Huang X., Yoshino K., Nakao H., Takeda T.;
 RT "Nucleotide sequence of a gene encoding the novel Versinia
 enterocolitica heat-stable enterotoxin that includes a pro-region-like
 sequence in its mature toxin molecule.";
 RL Microb. Pathog. 22:89-97(1997).
 RN (2)
 RP SEQUENCE OF 20-72.
 RC STRAIN=Serotype O:3;
 RX MEDLINE=95246844; PubMed=7729521; DOI=10.1016/0014-5793(95)00267-D;
 RA Yoshino K., Takeda T., Huang X., Murata H., Nakao H., Takeda T.,
 RA Shimonishi Y.;
 RT "Characterization of a highly toxic, large molecular size heat-stable
 enterotoxin produced by a clinical isolate of Versinia
 enterocolitica";
 RL FEMS Lett. 362:319-322(1995).
 CC -!- FUNCTION: Toxin which activates the particulate form of guanylate
 cyclase and increases cyclic GMP levels within the host intestinal
 epithelial cells. Highly toxic.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
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 CC -----
 DR EMBL; D63578; BAA23656.1; -;
 DR HSSP; P01559; 1ETN.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1_
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 KW Direct protein sequencing; Enterotoxin; Signal; Toxin.
 FT SIGNAL 1 19
 FT CHAIN 20 72 Heat-stable enterotoxin C.
 FT DISULFID 60 65 By similarity.
 FT DISULFID 61 69 By similarity.
 FT DISULFID 64 72 By similarity.
 SQ SEQUENCE 72 AA; 7639 MW; 7C0D83893C2F981D CRC64;
 Query Match 52.6%; Score 10; DB 1; Length 72;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 6 CCELCNCPAC 15
 Db 60 CCELCNCPAC 69
 RESULT 10
 HST_YERKR
 ID HST_YERKR STANDARD; PRT; 66 AA.
 AC P31518;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat-stable enterotoxin precursor.

GN Name=yst;
 OS Yersinia kristensenii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=28152;
 RN (1) SEQUENCE FROM N.A.
 RP STRAIN=IP490 / Serotype O:12,25;
 RC STRAIN=IP490 / Serotype O:12,25;
 RA Ibrahim A., Liesack W., Stackebrandt E.;
 RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Toxin which activates the particulate form of guanylate
 cyclase and increases cyclic GMP levels within the host intestinal
 epithelial cells (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
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 CC -----
 DR EMBL; X69218; CAA49152.1; -;
 DR PIR; S31652; S31652.
 DR HSSP; P01559; 1ETN.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1_
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 KW Enterotoxin; Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 50 Heat-stable enterotoxin (By similarity).
 FT DISULFID 51 56 By similarity.
 FT DISULFID 54 59 By similarity.
 FT DISULFID 55 63 By similarity.
 FT DISULFID 58 66 By similarity.
 SQ SEQUENCE 66 AA; 7068 MW; 27BE7006675CC075 CRC64;
 Query Match 47.4%; Score 9; DB 1; Length 66;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 10 CCNPACAGC 18
 Db 58 CCNPACAGC 66
 RESULT 11
 HSTA_YEREN
 ID HSTA_YEREN STANDARD; PRT; 71 AA.
 AC P07593;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat-stable enterotoxin A precursor (YST-A).
 GN Name=ystA; Synonyms=yst;
 OS Yersinia enterocolitica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=630;
 RN (1) SEQUENCE FROM N.A.
 RP STRAIN=Serotype O:8;
 RC MEDLINE=93051243; PubMed=1427005; DOI=10.1016/0378-1097(92)90364-T;
 RA Ibrahim A., Liesack W., Pike S., Stackebrandt E.;
 RT "The polymerase chain reaction: an epidemiological tool to
 differentiate between two clusters of pathogenic Yersinia
 enterocolitica strains";
 RL FEMS Microbiol. Lett. 76:63-66(1992).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=W1024 / Serotype O:9;
 DE Heat-stable enterotoxin precursor.

RX MEDLINE=90354067; PubMed=2201642;
 RA Delor I., Kaeckenbeek A., Wauters G., Cornelis G.R.;
 RT "Nucleotide sequence of yst, the Yersinia enterocolitica gene encoding
 the heat-stable enterotoxin, and prevalence of the gene among
 pathogenic and nonpathogenic yersiniae."; Infect. Immun. 58:2983-2988(1990).
 RL Infect. Immun. 58:2983-2988(1990).
 RN [3]
 RP SEQUENCE OF 54-71.
 RX MEDLINE=86004705; PubMed=4043080;
 RA Takao T., Tomimaga N., Yoshimura S., Shimonishi Y., Hara S., Inoue T.,
 RA Miyama A.;
 RT "Isolation, primary structure and synthesis of heat-stable enterotoxin
 produced by Yersinia enterocolitica."; Eur. J. Biochem. 152:199-206(1985).
 RL Eur. J. Biochem. 152:199-206(1985).
 CC -1- FUNCTION: Toxin which activates the particulate form of guanylate
 cyclase and increases cyclic GMP levels within the host intestinal
 epithelial cells.
 CC -1- SUBCELLULAR LOCATION: Secreted.
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 CC -----
 DR ENBL; X65999; CAA46801.1; -;
 DR ENBL; U09235; AAA18472.1; -;
 DR PIR; S25659; S25659.
 DR HSSP; P01559; IETN.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin_H_STABLE; 1.
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 KW Direct protein sequencing; Enterotoxin; Signal; Toxin.
 FT SIGNAL 1 19 Potential.
 FT PROPEP 20 53 Heat-stable enterotoxin A.
 FT CHAIN 54 71 By similarity.
 FT DISULFID 59 64 By similarity.
 FT DISULFID 60 68 By similarity.
 FT DISULFID 63 71 By similarity.
 FT VARIANT 48 48 L -> S.
 SQ SEQUENCE 71 AA; 7494 MW; 022F99B3800C861B CRC64;
 Query Match 47.4%; Score 9; DB 1; Length 71;
 Best Local Similarity 100.0%; Pred. No. 0.0047;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 CCNPACAGC 18
 Db 63 CCNPACAGC 71
 RESULT 12
 HSTB_YEREN STANDARD; PRT; 71 AA.
 AC P7497;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat-stable enterotoxin B precursor (Y-STB).
 GN Names=YSTB;
 OS Yersinia enterocolitica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=630;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=84-50 / Serotype O:5;
 RX MEDLINE=98008784; PubMed=9344780; DOI=10.1006/mpat.1997.0146;
 RA Ramamurthy T., Yoshino K., Huang X., Nair G.B., Carniel E.,
 RA Maruyama T., Fukushima H., Takeda T.;
 RT "The novel heat-stable enterotoxin subtype gene (ystB) of Yersinia
 enterocolitica: nucleotide sequence and distribution of the yst
 genes."; Microb. Pathog. 23:199-200(1997).
 RL Microb. Pathog. 23:199-200(1997).
 CC -1- FUNCTION: Toxin which activates the particulate form of guanylate
 cyclase and increases cyclic GMP levels within the host intestinal
 epithelial cells. Could play an important role in pathogenesis.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.
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 CC -----
 DR ENBL; D88145; BAA13544.1; -;
 DR HSSP; P01559; IETN.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin_H_STABLE; 1.
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 KW Direct protein sequencing; Enterotoxin; Signal; Toxin.
 FT SIGNAL 1 19 Potential.
 FT PROPEP 20 52 Heat-stable enterotoxin B.
 FT CHAIN 53 71 By similarity.
 FT DISULFID 59 64 By similarity.
 FT DISULFID 60 68 By similarity.
 FT DISULFID 63 71 By similarity.
 SQ SEQUENCE 71 AA; 7670 MW; ED6E9F61ACDD4F50 CRC64;
 Query Match 47.4%; Score 9; DB 1; Length 71;
 Best Local Similarity 100.0%; Pred. No. 0.0047;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 CCNPACAGC 18
 Db 63 CCNPACAGC 71
 RESULT 13
 CXAA_CONGE STANDARD; PRT; 15 AA.
 ID CXAA_CONGE
 AC P01519;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alpha-conotoxin GIA [contains: Alpha-conotoxin GI (G1)].
 OS Conus geographus (Geography cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6491;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81191854; PubMed=7014556;
 RA Gray W.R., Luque F.A., Olivera B.M., Barrett J., Cruz L.J.;
 RT "Peptide toxins from Conus geographus venom."; J. Biol. Chem. 256:4734-4740(1981).
 RL J. Biol. Chem. 256:4734-4740(1981).
 RN [2]
 RP DISULFIDE BONDS OF GI, AND SYNTHESIS OF GI.
 RX MEDLINE=83105694; PubMed=7152021; DOI=10.1016/0014-5793(82)80820-X;
 RA Nishiuchi Y., Sakakibara S.;
 RT "Primary and secondary structure of conotoxin GI, a neurotoxic
 tridecapeptide from a marine snail."; FEBS Lett. 148:260-262(1982).
 RL FEBS Lett. 148:260-262(1982).
 RN [3]
 RP DISULFIDE BONDS OF GI, AND SYNTHESIS OF GI.

RT MEDLINE=84280842; PubMed=6466616;
RA Gray W.R., Luque F.A., Galyean R., Atherton E., Sheppard R.C.,
RA Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M., Cruz L.J.,
RA Rivier J.;
RT "Conotoxin GI: disulfide bridges, synthesis, and preparation of
RT iodinated derivatives.";
RL Biochemistry 23:2796-2802(1984).
[4]
RP COMPARISON WITH ALPHA-CONOTOXIN SI AND ALPHA-CONOTOXIN MI.
RX MEDLINE=95034849; PubMed=7947815;
RA Hann R.M., Pagan O.R., Eterovic V.A.;
RT "The alpha-conotoxins GI and MI distinguish between the nicotinic
RT acetylcholine receptor agonist sites while SI does not.";
RL Biochemistry 33:14058-14063(1994).
[5]
RP PHARMACOLOGICAL CHARACTERIZATION ON MOUSE MUSCLE-DERIVED BC3H-1 CELLS
RX MEDLINE=95349531; PubMed=7623764;
RA Groebe D.R., Dumm J.M., Levitan E.S., Abramson S.N.;
RT "alpha-Conotoxins selectively inhibit one of the two acetylcholine
RT binding sites of nicotinic receptors.";
RL Mol. Pharmacol. 48:105-111(1995).
[6]
RP MUTAGENESIS OF ARG-9.
RX MEDLINE=97317090; PubMed=9174364; DOI=10.1021/bi970195w;
RA Groebe D.R., Gray W.R., Abramson S.N.;
RT "Determinants involved in the affinity of alpha-conotoxins GI and SI
RT for the muscle subtype of nicotinic acetylcholine receptors.";
RL Biochemistry 36:8469-8474(1997).
[7]
RP X-RAY CRYSTALLOGRAPHY (1.2 ANGSTROMS) OF GI.
RX MEDLINE=96378624; PubMed=8784187; DOI=10.1021/bi960820h;
RA Guddat L.W., Martin J.A., Shan L., Edmundson A.B., Gray W.R.;
RT "Three-dimensional structure of the alpha-conotoxin GI at 1.2-A
RT resolution.";
RL Biochemistry 35:11329-11335(1996).
[8]
RP STRUCTURE BY NMR OF GI.
RX MEDLINE=89152562; PubMed=2765514;
RA Kobayashi Y., Ohkubo T., Kyogoku Y., Nishiuchi Y., Sakakibara S.,
RA Braun W., Go N.;
RT "Solution conformation of conotoxin GI determined by 1H nuclear
RT magnetic resonance spectroscopy and distance geometry calculations.";
RL Biochemistry 28:4853-4860(1989).
[9]
RP STRUCTURE BY NMR OF GI.
RX MEDLINE=89375269; PubMed=2775719;
RA Pardi A., Gaides A., Fiorance J., Manicote D.;
RT "Solution structures of alpha-conotoxin GI determined by two-
RT dimensional NMR spectroscopy.";
RL Biochemistry 28:5494-5501(1989).
[10]
RP STRUCTURE BY NMR OF GI.
RX MEDLINE=98321613; PubMed=9660176;
RA Maslennikov I.V., Sobol A.G., Gladky K.V., Lugovskoy A.A.,
RA Ostrovsky A.G., Tsetlin V.I., Ivanov V.T., Arseniev A.S.;
RT "Two distinct structures of alpha-conotoxin GI in aqueous solution.";
RL Eur. J. Biochem. 254:238-247(1998).
[11]
RP STRUCTURE BY NMR OF GI.
RX MEDLINE=98239743; PubMed=9571060; DOI=10.1006/jmbi.1998.1701;
RA Gehrmann J., Alewood P.F., Craik D.J.;
RT "Structure determination of the three disulfide bond isomers of alpha-
RT conotoxin GI: a model for the role of disulfide bonds in structural
RT stability.";
RL J. Mol. Biol. 278:401-415(1998).
[12]
RP STRUCTURE BY NMR OF AN ANTITOXIC ANALOG OF GI.
RX MEDLINE=99438341; PubMed=10508392; DOI=10.1021/bi990558n;
RA Mok K.H., Han K.H.;
RT "NMR solution conformation of an antitoxic analogue of alpha-conotoxin
RT GI: identification of a common nicotinic acetylcholine receptor
RT alpha(1)-subunit binding surface for small ligands and alpha-

RT conotoxins.";
RL Biochemistry 38:11895-11904(1999).
CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them. The higher affinity site for alpha-conotoxin GI is
CC the alpha/delta site on mouse muscle-derived BC3H-1 receptor, and
CC the other site (alpha/gamma site) on nicotinic receptors from
CC Torpedo californica electric organ.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
CC family.
DR PIR; A01782; NTRNAG.
DR PDB; 1NOT; X-ray; @=1-14.
DR PDB; 1QS3; NMR; A=2-13.
DR PDB; 1XGA; NMR; @=1-14.
DR PDB; 1XGB; NMR; @=1-14.
DR PDB; 1XGC; NMR; @=1-14.
KW 3D-structure; Acetylcholine receptor inhibitor; Amidation;
KW Direct protein sequencing; Neurotoxin; Postsynaptic neurotoxin; Toxin.
FT PEPTIDE 1 15 Alpha-conotoxin GIA.
FT 1 13 Alpha-conotoxin GI.
FT DISULFID 2 7
FT DISULFID 3 13
FT MOD_RES 13 13
FT MOD_RES 15 15 Cysteine amide (G-14 provides amide
FT MUTAGEN 9 9 group) (in alpha-conotoxin GI).
FT STRAND 2 2 Lysine amide (in alpha-conotoxin GIA).
FT HELIX 5 10 R->A: Reduction in affinity for both
FT STRAND 12 12 alpha/delta and alpha/gamma sites on
FT SEQUENCE 15 AA; 1628 MW; 2AE73EE90F8C2B19 CRC64; Torpedo receptors (in GI).
Query Match 31.6%; Score 6; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 CCNPAC 15
Db 2 CCNPAC 7
RESULT 14
Q9R581 PRELIMINARY; PRT; 17 AA.
AC Q9R581;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 01-ST-1, NAG-ST, VM-ST=HEAT-stable enterotoxin.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE.
RX MEDLINE=93314823; PubMed=8325391; DOI=10.1016/0014-5793(93)81766-S;
RA Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
RA Takeda T., Shimonishi Y.;
RT "Purification and sequence determination of heat-stable enterotoxin
RT elaborated by a cholera toxin-producing strain of Vibrio cholerae
RT O1.";
RL FEBS Lett. 326:83-86(1993).
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN H STABLE; 1.
DR SEQUENCE 17 AA; 1821 MW; 30FF036D018D601C CRC64;

Query Match 31.6%; Score 6; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCNPAC 15
Db 7 CCNPAC 12

RESULT 15

Q9R580 PRELIMINARY; PRT; 18 AA.
AC Q9R580;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 01-St-2, VC-H-St=HEAT-stable enterotoxin.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE.
RX MEDLINE=93314823; PubMed=8325391; DOI=10.1016/0014-5793(93)81766-S;
RA Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
RA Takeda T., Shimonishi Y.;
RT "Purification and sequence determination of heat-stable enterotoxin
RT elaborated by a cholera toxin-producing strain of Vibrio cholerae
RT O1,"
RL FEBS Lett. 326:83-86(1993).
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin_HS.
DR Pfam; PF02048; Enterotoxin_HS; I.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
SQ SEQUENCE 18 AA; 1934 MW; 3080692D018D601C CRC64;

Query Match 31.6%; Score 6; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCNPAC 15
Db 8 CCNPAC 13

Search completed: March 26, 2005, 17:24:50
Job time : 75.9821 secs

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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:49:45 ; Search time 80.0357 Seconds
(without alignments)
86.982 Million cell updates/sec

Title: US-10-775-481A-3

Perfect score: 18
Sequence: 1 NTFYCCCLCCYPACAGCN 18

Scoring table:  Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	1 AAP40186	Aap40186 Sequence
2	18	100.0	18	2 AAR85967	Aar85967 ST I* rec
3	18	100.0	18	2 AAY40529	Aay40529 ST recept
4	18	100.0	18	5 AAU93984	Aau93984 E. coli S
5	18	100.0	18	7 ADE10846	Adel10846 Chimeric
6	18	100.0	18	7 ADM39751	Adm39751 Escherich
7	18	100.0	18	8 ADG63946	Adg63946 Recombina
8	18	100.0	18	8 ADP73480	Adp73480 Escherich
9	18	100.0	18	8 ADR12773	Adr12773 E. coli S
10	18	100.0	18	8 ADR48343	Adr48343 Bacterial
11	18	100.0	18	8 ADR48331	Adr48331 E. coli S
12	18	100.0	18	8 ADR45823	Adr45823 Amino aci
13	18	100.0	36	1 AAP30263	Aap30263 Sequence
14	17	94.4	17	2 AAR85966	Aar85966 ST I* rec
15	17	94.4	17	2 AAR85961	Aar85961 ST I* rec
16	17	94.4	17	2 AAY40528	Aay40528 ST recept
17	17	94.4	17	2 AAY40523	Aay40523 ST recept
18	17	94.4	17	8 ADR45837	Adr45837 Amino aci
19	17	94.4	17	8 ADR45842	Adr45842 Amino aci
20	16	88.9	16	2 AAR85962	Aar85962 ST I* rec
21	16	88.9	16	2 AAR85967	Aar85967 ST I* rec
22	16	88.9	16	2 AAY40524	Aay40524 ST recept
23	16	88.9	16	2 AAY40529	Aay40529 ST recept
24	16	88.9	16	8 ADR45838	Adr45838 Amino aci
25	16	88.9	16	8 ADR45843	Adr45843 Amino aci

26	15	83.3	15	2 AAR85968	Aar85968 ST I* rec
27	15	83.3	15	2 AAR85963	Aar85963 ST I* rec
28	15	83.3	15	2 AAY40525	Aay40525 ST recept
29	15	83.3	15	2 AAY40530	Aay40530 ST recept
30	15	83.3	15	8 ADR45844	Adr45844 Amino aci
31	15	83.3	15	8 ADR45839	Adr45839 Amino aci
32	15	83.3	18	5 AAU93985	Aau93985 E. coli S
33	15	83.3	18	7 ADE10847	Adel10847 Chimeric
34	15	83.3	18	7 ADM39752	Adm39752 Escherich
35	15	83.3	18	8 ADG63947	Adg63947 Recombina
36	15	83.3	18	8 ADP73481	Adp73481 Escherich
37	15	83.3	18	8 ADR12774	Adr12774 E. coli S
38	14	77.8	14	2 AAR85964	Aar85964 ST I* rec
39	14	77.8	14	2 AAR85969	Aar85969 ST I* rec
40	14	77.8	14	2 AAY40531	Aay40531 ST recept
41	14	77.8	14	2 AAY40526	Aay40526 ST recept
42	14	77.8	14	5 AAU93983	Aau93983 E. coli S
43	14	77.8	14	7 ADE10845	Adel10845 Chimeric
44	14	77.8	14	7 ADM39750	Adm39750 Escherich
45	14	77.8	14	8 ADG63945	Adg63945 Recombina

ALIGNMENTS

RESULT 1

AAP40186
ID AAP40186 standard; peptide; 18 AA.

AC AAP40186;

XX 25-MAR-2003 (revised)

DT 04-FEB-1992 (first entry)

XX Sequence of monomeric synthetic heat-stable Escherichia coli enterotoxin

DE IB analogue VII.

XX Vaccine; diarrhoea; diagnosis; antigen.

OS Escherichia coli.

XX W08402700-A.

PD 19-JUL-1984.

PF 21-DEC-1983; 83WO-US002008.

XX 03-JAN-1983; 83US-00455265.

PR 12-DEC-1983; 83US-00559469.

PR 12-DEC-1984; 84WO-US002030.

(SCRI) SCRIPPS CLINIC & RES FOUND.

XX Houghten RA;

PI WPI; 1984-188753/30.

DR Synthetic polypeptide(s) with antigenicity of E.coli enterotoxin - useful

XX for vaccination against diarrhoea and for diagnostic tests.

PT Example; Page 53; 177pp; English.

XX The peptides of the invention can be used in a vaccine useful for

CC conferring protection against diarrhoea. They may also be used in a

CC diagnostic or reagent system for assaying for infections caused by the

CC E.coli strains. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 18 AA;

SQ Query Match 100.0%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 NTFYCCCLCCYPACAGCN 18
Db      1 NTFYCCCLCCYPACAGCN 18

RESULT 2
AAR85947
ID AAR85947 standard; peptide; 18 AA.
XX
AC AAR85947;
XX
DT 19-JAN-1996 (first entry)
XX
DE ST I* receptor ligand portion.
XX
KW ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
KW colorectal; metastasis.
XX
OS Escherichia coli.
XX
PN W09511694-A1.
XX
PD 04-MAY-1995.
XX
PF 26-OCT-1994; 94WO-US012232.
XX
PR 26-OCT-1993; 93US-00141892.
PR 13-SEP-1994; 94US-00305056.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Waldman SA;
XX
DR WPI; 1995-178646/23.
XX
DT Conjugated cpds. which specifically bind to colorectal cancer cells -
PT comprise heat-stable toxin receptor binding moiety and active moiety
PT which may be a therapeutic agent or a radioactive agent.
XX
PS Claim 3; Page 116; 133pp; English.
XX
CC New conjugated compounds are provided which consist of (1) an ST receptor
CC binding moiety and (2) an active moiety which is a radio- stable agent.
CC 'ST' refers to a heat stable toxin produced by E.coli and other
CC organisms. Especially the radiostable agent is a therapeutic agent (e.g.
CC methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive
CC isotope) or nucleic acid; and the compound is used for the detection,
CC imaging or treatment of colorectal tumours, particularly metastasised
CC tumours. The present sequence is a specific example of an ST receptor
CC binding peptide which can be used in the conjugate
XX
SQ Sequence 18 AA;

Query Match      100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NTFYCCCLCCYPACAGCN 18
Db      1 NTFYCCCLCCYPACAGCN 18

RESULT 4
AAU93984
ID AAU93984 standard; peptide; 18 AA.
XX
AC AAU93984;
XX
DT 02-JUL-2002 (first entry)
XX
DE E. coli ST B cell epitope #2.
XX
KW Immunogenic; hepadnavirus nucleocapsid protein; hepatitis B core; HBc;
KW vaccine; B cell epitope; T cell epitope; immunostimulant.
XX
OS Escherichia coli.
XX
PN W0200214478-A2.
XX
PD 21-FEB-2002.
XX
PF 16-AUG-2001; 2001WO-US041759.
XX
PR 16-AUG-2000; 2000US-0225843P.
PR 22-AUG-2000; 2000US-0226867P.
PR 15-AUG-2001; 2001US-00930915.
XX
PA (APOV-) APOVIA INC.
XX
PI Birkett AJ;
XX
DR WPI; 2002-257601/30.
XX

```

PT Novel recombinant hepatitis B core protein, termed as chimeric
 PT hepatitis B core protein, displays immunogenic epitopes at N-terminus,
 PT HBC immunogenic loop with linker for conjugated epitope and C-terminus.
 XX
 PS Disclosure; Page 38; 289pp; English.
 XX
 CC The invention relates to a recombinant hepatitis B core protein,
 CC i.e. a chimeric hepatitis B core (HBC) protein (I), displaying one or
 CC more immunogenic epitopes at the N-terminus, HBC immunogenic loop (L) or
 CC C-terminus, or having a heterologous linker for a conjugated epitope in
 CC (L), and containing a Cys residue at, or near, the C-terminus that
 CC confers enhanced stability to the particles. A vaccine comprising (I) is
 CC useful for inducing an immune response in an inoculated host animal, by
 CC inoculating a host animal with the vaccine, and maintaining that
 CC inoculated animal for a time period sufficient for that animal to develop
 CC an immune response. The immunogenic particles formed using (I) are
 CC substantially free of binding to nucleic acids, and are most stable than
 CC the particle formed from otherwise identical HBC chimer that lacks the C-
 CC terminal residue or in which a C-terminal Cys is replaced by another
 CC residue. The chimer particles are most stable on storage in aqueous
 CC compositions that are particles of similar sequence that lack any C-
 CC terminal Cys residues. The chimer molecule exhibits the self-assembly not
 CC exhibiting the nucleic acid binding of those native particles, and
 CC excellent B cell and T cell immunogenicities. The chimer particles are
 CC typically prepared in higher yield than similar particles that are free
 CC of a C-terminal Cys. The particles are often far more immunogenic than
 CC the similar conjugates that lack a C-terminal Cys. Immunogenicities of
 CC particles assembled from the chimer molecules are enhanced as compared to
 CC similar particles assembled from chimer molecules lacking at least one C-
 CC terminal Cys. AAU93802-AAU93997 represent immunogenic HBC particles amino
 CC acid sequences and related sequences of the invention
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 18; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCELCYCPACAGCN 18
 |||||
 Db 1 NTFYCCELCYCPACAGCN 18

RESULT 5
 ADE10846
 ID ADE10846 standard; peptide; 18 AA.

XX AC ADE10846;

XX DT 29-JAN-2004 (first entry)

XX DE Chimeric hepatitis B virus related B-cell epitope seqid 80.

XX KW hepatotropic; virucide; antiinflammatory; chronic hepatitis; vaccine;
 KW recombinant hepatitis B core chimeric protein; HBC chimeric protein;
 KW hepatitis B infection; T-cell stimulator; B-cell epitope.

XX OS Escherichia coli.

XX PN US2003198645-A1.

XX PD 23-OCT-2003.

XX PF 21-FEB-2003; 2003US-00372076.

XX PR 21-FEB-2002; 2002US-00080299.

XX PR 21-FEB-2002; 2002US-00082014.

XX (PAGE/) PAGE M.

XX PA (FRIE/) FRIEDE M.

XX PI Page M, Friede M;

XX

DR WPI; 2003-852775/79.

XX Treating chronic hepatitis B infection by administering a T cell-
 PT stimulating vaccine containing immunogenic particles having recombinant
 PT carboxy-terminal truncated hepatitis B core (HBC) chimeric protein
 PT molecules.

XX Disclosure; SEQ ID NO 80; 111pp; English.

PS The invention describes a method of treating chronic hepatitis comprising
 XX administering to a patient a T cell-stimulating amount of a vaccine
 CC comprising immunogenic particles dissolved or dispersed in a diluent,
 CC where the immunogenic particles consists of recombinant hepatitis B core
 CC (HBC) chimeric protein molecules, and maintaining the patient to induce T
 CC cells activated against HBC. The methods and compositions of the present
 CC invention are useful for treating chronic hepatitis B infection. This is
 CC the amino acid sequence of a chimeric hepatitis B virus related B-cell
 CC epitope useful for expression within the HBV chimer at the N-terminus,
 CC within the immunogenic loop and/or at the C-terminus.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 7; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCELCYCPACAGCN 18
 |||||
 Db 1 NTFYCCELCYCPACAGCN 18

RESULT 6

ADM39751

ID ADM39751 standard; peptide; 18 AA.

XX AC ADM39751;

XX DT 03-JUN-2004 (first entry)

XX DE Escherichia coli B-cell peptide epitope expressed by HBC chimer Seq 83.

XX KW immunogenic; avian hepatitis B virus; nucleocapsid;

XX KW self assembled particle; immunogen; inoculum; vaccine; immunostimulant;
 KW antibacterial; virucidal; B-cell epitope.

XX OS Escherichia coli.

XX PN WO2003072722-A2.

XX PD 04-SEP-2003.

XX PF 21-FEB-2003; 2003WO-US005315.

XX PR 21-FEB-2002; 2002US-0359129P.

XX PA (APOV-) APOVIA INC.

XX PI Birkett AJ, Peck B;

XX DR WPI; 2003-679948/64.

XX New recombinant chimer avian hepatitis B core protein molecule, useful as
 PT an immunogen for inducing a B cell or T cell response to produce
 PT antibodies, or as a vaccine against pathogens.

XX Disclosure; SEQ ID NO 83; 278pp; English.

XX This invention relates to novel recombinant immunogenic chimeric avian
 CC hepatitis B core (AHBC) nucleocapsid proteins. Specifically, it refers to
 CC an AHBC protein that has been engineered to display an immunogenic B cell
 CC or T cell epitope, exhibit enhanced stability and an absence of nucleic
 CC acid binding as a self assembled particle. The present invention
 CC describes the chimeric AHBC protein as truncated at the C-terminus and

CC containing introduced cysteine residues that confers an enhanced
 CC stability in aqueous solution, an increased yield and more immunogenicity
 CC than similar conjugates that lack N- or C-terminal cysteines.
 CC Furthermore, a reduction in the number of positively charged residues
 CC (lysine and arginine) towards the C-terminus prepares self-assembled
 CC particles that are substantially free of nucleic acid binding. As such,
 CC these chimeric particles can be used as immunogens of an inoculum that
 CC induce a B cell or T cell response in an animal to produce antibodies. It
 CC can also be useful for developing a vaccine to protect against the
 CC pathogen from which the heterologous epitope or the haptan is derived.
 CC Accordingly, these compositions exhibit immunostimulant, antibacterial
 CC and virucidal activities. This peptide sequence is an exemplary B-cell
 CC epitope peptide immunogen useful for both linkage to the linker residue
 CC after expression of a contemplated chimera and for expression within an
 CC HBC chimera of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 7; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACACGN 18
 |||||
 Db 1 NTFYCCCLCCYPACACGN 18

RESULT 7

ADG63946
 ID ADG63946 standard; peptide; 18 AA.

XX AC ADG63946;

XX DT 11-MAR-2004 (first entry)

XX DE Recombinant chimera hepatitis B core protein immunogenic epitope #71.
 XX KW Recombinant chimera hepatitis B core protein; HBC; immunogenic epitope;
 XX KM HBC immunodominant loop; immune response.

XX OS Escherichia coli.

XX PN US2003185858-A1.

XX PD 02-OCT-2003.

XX PF 21-FEB-2002; 2002US-00082014.

XX PR 15-AUG-2001; 2001US-00930915.

XX PA (BIRK/) BIRKETT A J.

XX PI Birkett AJ;

XX DR WPI; 2004-031988/03.

XX PT Recombinant chimera hepatitis B core protein molecule useful for preparing
 PT vaccine or inoculum includes peptide-bonded heterologous immunogenic
 PT epitope at N-terminus in the hepatitis B core immunodominant loop or C-
 PT terminus of the chimera.

XX PS Disclosure; SEQ ID NO 79; 110pp; English.

XX CC The invention relates to a recombinant chimera hepatitis B core (HBC)
 CC protein molecule that includes a peptide-bonded heterologous immunogenic
 CC epitope at the N-terminus in the HBC immunodominant loop or the C-
 CC terminus of the chimera, or a heterologous linker residue to a conjugated
 CC epitope present in the loop. The invention also relates to an immunogenic
 CC particle comprising the recombinant hepatitis B core chimera protein
 CC molecules, a vaccine comprising the immunogenic particles dissolved or
 CC dispersed in a diluent, a nucleic acid that encodes a recombinant HBC
 CC protein molecule or its variant, analogue, or complement and a method for
 CC inducing an immune response in an inoculated host animal comprising

CC inoculating a host animal with a vaccine and maintaining the inoculated
 CC animal for a period of time sufficient to enable development of an immune
 CC response. The recombinant chimera hepatitis B core protein molecule is
 CC used in an immunogenic particle for preparing a vaccine useful for
 CC inducing an immune response in an inoculated host animal. This sequence
 CC represents an HBC protein immunogenic B cell epitope of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACACGN 18
 |||||
 Db 1 NTFYCCCLCCYPACACGN 18

RESULT 8

ADP73480
 ID ADP73480 standard; peptide; 18 AA.

XX AC ADP73480;

XX DT 09-SEP-2004 (first entry)

XX DE Escherichia coli B cell epitope of gene ST, SEQ ID 93.

XX KW transgenic animal; Hepatitis B virus nucleocapsid core protein; HBC;
 XX KM enhanced stability; hepatotropic; virucide; immunology;
 XX KW protein engineering; immunogen; vaccine; Hepatitis B infection.

XX OS Escherichia coli.

XX PN WO2004053091-A2.

XX PD 24-JUN-2004.

XX PF 10-DEC-2003; 2003WO-US039164.

XX PR 10-DEC-2002; 2002US-0432123P.

XX PA (APOV-) APOVIA INC.

XX PI Lyons K, Birkett AJ, Haron JA;

XX DR WPI; 2004-468859/44.

XX PT New recombinant chimera hepatitis B core (HBC) protein molecules useful in
 PT the fields of immunology and protein engineering, in particular as an
 PT immunogen in a vaccine for Hepatitis B infections.

XX PS Disclosure; SEQ ID NO 93; 338pp; English.

XX CC The invention relates to a novel recombinant chimera hepatitis B virus
 CC nucleocapsid (core) protein (HBC), up to 600 or 380 amino acid residues
 CC in length. The chimera protein is engineered for both enhanced stability
 CC of self-assembled particles and the substantial absence of nucleic acid
 CC binding by the particles. The invention further comprises: a recombinant
 CC HBC protein chimera molecule that has a length of 135-365 amino acid
 CC residues and contains four peptide-linked amino acid residue sequence
 CC domains from the N-terminus that are denominated Domains I, II, III and
 CC IV. The invention also provides nucleic acids, polypeptides, host cells,
 CC vectors and transgenic animals used in the methods of the invention. The
 CC chimeric compositions of the invention have hepatotropic and virucide
 CC activities. The methods and compositions of the present invention are
 CC useful in the fields of immunology and protein engineering, in particular
 CC for using a chimera hepatitis B virus nucleocapsid protein as an
 CC immunogen in a vaccine for Hepatitis B infections. This sequence
 CC represents a Hepatitis B virus nucleocapsid (core) protein related
 CC polypeptide of the invention.

XX Sequence 18 AA;

Query Match	100.0%;	Score 18;	DB 8;	Length 18;
Best Local Similarity	100.0%;	Pred. No. 1.3e-12;		
Matches	18;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	NTFYCCCLCCYPACAGCN 18		
Dd	1	NTFYCCCLCCYPACAGCN 18		
RESULT 9				
ADRI2773		ADRI2773 standard; peptide; 18 AA.		
XX	AC	ADRI2773;		
XX	AC			
DT	DT	04-NOV-2004 (first entry)		
XX	XX	E. coli ST B cell epitope #2.		
DE	DE			
XX	XX	HBV; chronic hepatitis; Hbc; nucleocapsid core protein; vaccine;		
KW	KW	immunogen; immunogenic epitope; T cell; B cell; CD8+ cell; CD4+ cell;		
KW	KW	cytotoxic T lymphocyte; toll-like receptor 4; toll-like receptor 9;		
KW	KW	TLR-4; TLR-9; epitope.		
XX	XX			
OS	OS	Escherichia coli.		
XX	XX			
PN	PN	US2004156863-A1.		
XX	XX			
PD	PD	12-AUG-2004.		
XX	XX			
PF	PF	01-OCT-2003; 2003US-00677074.		
XX	XX			
PR	PR	21-FEB-2002; 2002US-00080399.		
PR	PR	21-FEB-2002; 2002US-00082014.		
PR	PR	21-FEB-2003; 2003US-00372076.		
XX	XX			
PA	PA	(PAGE/) PAGE M.		
PA.	PA.	(FRIE/) FRIEDE M.		
PA	PA	(SCHM/) SCHMIDT A E.		
PA	PA	(STOB/) STOB D.		
XX	XX			
PI	PI	Page M, Friede M, Schmidt AE, Stober D;		
XX	XX			
DR	DR	WFI; 2004-603322/58.		
XX	XX			
PT	PT	Treating chronic hepatitis, by administering vaccine comprising		
PT	PT	immunogenic particles having recombinant hepatitis B core chimeric		
PT	PT	protein molecules, that stimulates T cell, to patient chronically		
PT	PT	infected with hepatitis B virus.		
XX	XX			
PS	PS	Disclosure; SEQ ID NO 80; 117pp; English.		
XX	XX			
CC	CC	The invention relates to treating chronic hepatitis, by administering a		
CC	CC	vaccine comprising immunogenic particles having recombinant hepatitis B		
CC	CC	core (Hbc) chimeric protein molecules (where truncated Hbc molecules are		
CC	CC	linked N-terminally or C-terminally to an immunogenic epitope), that		
CC	CC	stimulate T cell production, to a patient chronically infected with		
CC	CC	hepatitis B virus, and maintaining patient for time sufficient to induce		
CC	CC	T cells activated against Hbc. The chimeric proteins are still capable		
CC	CC	self-assembling into particles upon expression in a host cell and are		
CC	CC	substantially free of binding to nucleic acids, and the particles display		
CC	CC	enhanced stability. Also included is enhancing (M2) the production of one		
CC	CC	or more of gamma-producing CD8+, CD4+ T cells and cytotoxic T lymphocytes		
CC	CC	against hepatitis B virus, involving administering to a patient		
CC	CC	chronically infected with hepatitis B virus, a T cell-stimulating amount		
CC	CC	of a vaccine comprising immunogenic particles dissolved or dispersed in a		
CC	CC	diluent containing one or both of an agonist of toll-like receptor 4 and		
CC	CC	receptor 9 (TLR-4 and TLR-9), the immunogenic particles comprising Hbc		
CC	CC	chimeric protein molecules and maintaining the patient for a sufficient		
CC	CC	time to induce T cells activated against Hbc. The immunogenic epitopes		
CC	CC	may be B cell or T cell epitopes. The chimeric vaccine is useful for		
CC	CC	treating a patient chronically infected with hepatitis B virus. The		

CC disease. The peptide of the invention is also useful for treating
 CC obesity, congestive heart failure, cystic fibrosis or a patient suffering
 CC from constipation. The P1/GC-C receptor agonist is useful for treating
 CC cancer, respiratory disorder, neurological disorder, disorder associated
 CC with carbonate imbalance, erectile dysfunction, insulin-related disorder
 CC or inner ear disorder. P1 is useful in treating slow digestion or slow
 CC stomach emptying. P1 is useful in relieving symptoms of gastroparesis
 CC such as nausea, vomiting, bloating, and delayed gastric emptying. P1 is
 CC useful for treating or preventing asthma, nephritis, hepatitis,
 CC pancreatitis, allergies, etc. P1 is useful for treating or preventing
 CC type II diabetes mellitus, hyperglycaemia, respiratory disorders
 CC including inhalation. P1 is useful in treating or preventing retinopathy,
 CC nephropathy and edema formation. P1 is useful for treating or preventing
 CC headache, anxiety, sleep disorders and memory loss. P1 is useful as a
 CC marker to identify, detect, stage, or diagnosis diseases and conditions
 CC of the small intestine, including Crohn's disease, colitis, inflammatory
 CC bowel disease, tumours, etc. P1 can be conjugated to diagnostic or
 CC therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
 CC fibrosis lesions and specific cells lining the intestinal tract, thus
 CC useful in targeting radioactive moieties or therapeutic moieties to the
 CC intestine to aid in imaging and diagnosing or treating
 CC colorectal/metastasis or local colorectal cancer. The current sequence
 CC represents a bacterial ST peptide which is an activator of the GC-C
 CC receptor. ST peptides are considered super agonists of GC-C and are very
 CC resistant to proteolytic degradation.

SQ Sequence 18 AA;

Query Match 100.0%; Score 18; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTFYCCCLCCYPACAGCN 18
 DB 1 NTFYCCCLCCYPACAGCN 18

RESULT 11

ADR48331
 ID ADR48331 standard; peptide; 18 AA.

XX AC ADR48331;

XX DT 04-NOV-2004 (first entry)

XX DE E. coli ST I* peptide.

XX Gastrointestinal; antiinflammatory; laxative; cardiant; antitumor;
 KW anorectic; cardiovascular; cytostatic; analgesic; CNS; respiratory;
 KW neuroprotective; vasotropic; auditory; antiemetic; antiallergic;
 KW nephrotropic; hepatotropic; virucide; immunosuppressive; antiallergic;
 KW antidiabetic; ophthalmological; tranquiliser; hypnotic; nootropic;
 KW guanylate cyclase C; GC-C; receptor; gastrointestinal disorder;
 KW irritable bowel syndrome; constipation; gastroesophageal reflux disease;
 KW heartburn; dyspepsia; gastroparesis; Crohn's disease; ulcerative colitis;
 KW inflammatory bowel disease; obesity; heart failure; cystic fibrosis;
 KW cancer; respiratory disorder; neurological disorder; carbonate imbalance;
 KW erectile dysfunction; inner ear disorder; slow digestion; nausea;
 KW vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy;
 KW retinopathy; nephropathy; headache; anxiety; sleep disorder.

XX Escherichia coli.

XX OS

XX PN WO2004069165-A2.

XX PD 19-AUG-2004.

XX PF 28-JAN-2004; 2004WO-US002390.

XX PR 28-JAN-2003; 2003US-0443098P.

XX PR 15-MAY-2003; 2003US-0471288P.

XX PR 12-NOV-2003; 2003US-0519460P.

PA (MICR-) MICROBIA INC.

XX Currie MG, Mahajan-Miklos S;

XX WPI; 2004-604332/58.

DR Novel purified peptide capable of activating the guanylate cyclase C
 XX receptor, useful for treating obesity, congestive heart failure and
 PT benign prostatic hyperplasia.

XX Disclosure; Page 28; 93pp; English.

XX The invention relates to a purified peptide (P1) capable of activating
 CC the guanylate cyclase C (GC-C) receptor. Further disclosed is a
 CC pharmaceutical composition comprising the peptide of the invention. The
 CC composition of the invention is useful for treating a gastrointestinal
 CC disorder in a patient, which involves administering P1, where the
 CC gastrointestinal disorder is gastrointestinal motility disorder,
 CC irritable bowel syndrome, chronic constipation, a functional
 CC gastrointestinal disorder, gastroesophageal reflux disease, functional
 CC heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
 CC gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
 CC obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel
 CC disease. The peptide of the invention is also useful for treating
 CC obesity, congestive heart failure, cystic fibrosis or a patient suffering
 CC from constipation. The P1/GC-C receptor agonist is useful for treating
 CC cancer, respiratory disorder, neurological disorder, disorder associated
 CC with carbonate imbalance, erectile dysfunction, insulin-related disorder
 CC or inner ear disorder. P1 is useful in treating slow digestion or slow
 CC stomach emptying. P1 is useful in relieving symptoms of gastroparesis
 CC such as nausea, vomiting, bloating, and delayed gastric emptying. P1 is
 CC useful for treating or preventing asthma, nephritis, hepatitis,
 CC pancreatitis, allergies, etc. P1 is useful for treating or preventing
 CC type II diabetes mellitus, hyperglycaemia, respiratory disorders
 CC including inhalation. P1 is useful in treating or preventing retinopathy,
 CC nephropathy and edema formation. P1 is useful for treating or preventing
 CC headache, anxiety, sleep disorders and memory loss. P1 is useful as a
 CC marker to identify, detect, stage, or diagnosis diseases and conditions
 CC of the small intestine, including Crohn's disease, colitis, inflammatory
 CC bowel disease, tumours, etc. P1 can be conjugated to diagnostic or
 CC therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
 CC fibrosis lesions and specific cells lining the intestinal tract, thus
 CC useful in targeting radioactive moieties or therapeutic moieties to the
 CC intestine to aid in imaging and diagnosing or treating
 CC colorectal/metastasis or local colorectal cancer. The current sequence
 CC represents a bacterial ST peptide which is an activator of the GC-C
 CC receptor. ST peptides are considered super agonists of GC-C and are very
 CC resistant to proteolytic degradation.

SQ Sequence 18 AA;

Query Match 100.0%; Score 18; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTFYCCCLCCYPACAGCN 18

DB 1 NTFYCCCLCCYPACAGCN 18

RESULT 12

ADR45823

ID ADR45823 standard; peptide; 18 AA.

XX AC ADR45823;

XX DT 18-NOV-2004 (first entry)

XX DE Amino acid sequence of peptide ST I* inhibiting ST activity.

XX heat stable toxin; ST; ST receptor; colorectal cancer; gastric cancer;
 KW oesophageal cancer; colorectal cell; gastric cell; oesophageal cell;
 KW ST Ia.


```

XX OS Unidentified.
XX PN WO2004071436-A2.
XX PD 26-AUG-2004.
XX PF 10-FEB-2004; 2004WO-US003765.
XX PR 10-FEB-2003; 2003US-0446730P.
XX PA (UWJE-) UNIV JEFFERSON THOMAS.
XX PI Waldman SA, Pitari GM, Park J, Schulz S, Wolfe HR;
XX DR WPI; 2004-615913/59.
XX
XX Increasing ST receptor molecules on the surface of a colorectal, gastric
XX or esophageal cancer cell to treat these cancers comprises administering
XX ST receptor ligand molecules that bind to ST receptors on the surface of
XX the cancer cell.
XX
XX Claim 6; SEQ ID NO 3; 97pp; English.
XX
XX The specification describes a method for increasing the number of heat
XX stable toxin (ST) receptor molecules on the surface of a metastasised
XX colorectal cancer cell. The method comprises administering, by continuous
XX infusion, at least 0.1 nM of an ST receptor ligand per 10 kg bodyweight
XX per hour for at least 6 hours, where ST receptor ligand molecules bind to
XX ST receptors on the surface of the cancer cell in the individual and the
XX number of ST receptor molecules on the surface of the cancer cell is
XX increased. Therapeutic compositions comprising components which target ST
XX receptors can then be used to inhibit proliferation of the colorectal,
XX gastric and esophageal cells. This method may be used for treating
XX individuals that have diseases that affect colorectal, gastric and
XX esophageal cells, including colorectal, gastric or esophageal cancers.
XX The present sequence represents a peptide which inhibits ST activity, and
XX is designated ST I*. It is used as the ST receptor ligand in the method
XX of the invention.
XX
XX Sequence 18 AA;
XX
XX Query Match 100.0%; Score 18; DB 8; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-12;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 NTFYCCCLCCYPACAGCN 18
XX Db 1 NTFYCCCLCCYPACAGCN 18
XX
XX RESULT 13
XX AAP30263
XX ID AAP30263 standard; peptide; 36 AA.
XX AC AAP30263;
XX
XX 25-MAR-2003 (revised)
XX 25-APR-1992 (first entry)
XX
XX Sequence of peptide used to vaccinate against E. coli enterotoxin(s).
XX
XX Vaccine; enterotoxin; diarrhoea; immunogen.
XX
XX Escherichia coli.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 1..18
XX FT /label= Peptide P
XX
XX EP93652-A.
XX
XX 09-NOV-1983.
XX
XX 26-APR-1983; 83EP-00400827.
XX
XX 26-APR-1982; 82FR-00007179.
XX
XX (INSP ) INST PASTEUR.
XX (CNRS ) CENT NAT RECH SCI.
XX
XX Tartar A, Duflet E, Boquet P;
XX
XX WPI; 1983-816301/46.
XX
XX Peptide(s) used to vaccinate against E. coli enterotoxin(s) - contg. e.g.
XX asparagine threonine phenylalanine tyrosine cysteine glutamic
XX acid leucine cysteine asparagine sequences.
XX
XX Claim 1; Page 40; 50pp; French.
XX
XX The inventors claim peptides of formula (P)n (see FT; see also AAP30263)
XX having 4n-18n amino acids and pref. being laevorotatory (where n is 1 or
XX 2). In AAP30262 and AAP30263, N=2. When n is 2, the peptide comprises two
XX peptide sequences P, which may be the same or different, each having 4-18
XX amino acids chosen from the peptide P SQ in AAP30262 or AAP30263. The two
XX P sequences may be joined (a) by a disulphide bond or (b) by a bond
XX formed between a carboxyl gp. of one sequence of an amino gp. of the
XX other. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 36 AA;
XX
XX Query Match 100.0%; Score 18; DB 1; Length 36;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-12;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 NTFYCCCLCCYPACAGCN 18
XX Db 1 NTFYCCCLCCYPACAGCN 18
XX
XX RESULT 14
XX AAR85966
XX ID AAR85966 standard; peptide; 17 AA.
XX AC AAR85966;
XX
XX 19-JAN-1996 (first entry)
XX
XX ST I* receptor ligand portion.
XX
XX ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
XX colorectal; metastasis.
XX
XX Escherichia coli.
XX
XX WO9511694-A1.
XX
XX 04-MAY-1995.
XX
XX 26-OCT-1994; 94WO-US012232.
XX
XX 26-OCT-1993; 93US-00141892.
XX 13-SEP-1994; 94US-00305056.
XX
XX (UWJE-) UNIV JEFFERSON THOMAS.
XX
XX Waldman SA;
XX
XX WPI; 1995-178646/23.
XX
XX Conjugated cpds. which specifically bind to colorectal cancer cells -
XX comprise heat-stable toxin receptor binding moiety and active moiety
XX which may be a therapeutic agent or a radioactive agent.
XX
XX Claim 3; Page 120; 133pp; English.

```

XX New conjugated compounds are provided which consist of (1) an ST receptor
 CC binding moiety and (2) an active moiety which is a radio- stable agent.
 CC 'ST' refers to a heat stable toxin produced by E.coli and other
 CC organisms. Especially the radiostable agent is a therapeutic agent (e.g.
 CC methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive
 CC isotope) or nucleic acid; and the compound is used for the detection,
 CC imaging or treatment of colorectal tumours, particularly metastasised
 CC tumours. The present sequence is a specific example of an ST receptor
 CC binding peptide which can be used in the conjugate
 XX
 SQ Sequence 17 AA;

Query Match 94.4%; Score 17; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e-11;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TFCYCCCLCCYPACAGCN 18
 Db 1 TFCYCCCLCCYPACAGCN 17

RESULT 15

AAR85961
 ID AAR85961 standard; peptide; 17 AA.

XX
 AC AAR85961;

XX
 DT 19-JAN-1996 (first entry)

XX
 DE ST I* receptor ligand portion.

XX
 KW ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
 KW colorectal; metastasis.

XX
 OS Escherichia coli.

XX
 PN WO9511694-A1.

XX
 PD 04-MAY-1995.

XX
 PF 26-OCT-1994; 94WO-US012232.

XX
 PR 26-OCT-1993; 93US-00141892.

XX
 PR 13-SEP-1994; 94US-00305056.

XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.

XX
 PI Waldman SA;

XX
 WPI; 1995-178646/23.

XX Conjugated cpds. which specifically bind to colorectal cancer cells -
 PT comprise heat-stable toxin receptor binding moiety and active moiety
 PT which may be a therapeutic agent or a radioactive agent.

XX
 PS Claim 3; Page 119; 133pp; English.

XX New conjugated compounds are provided which consist of (1) an ST receptor
 CC binding moiety and (2) an active moiety which is a radio- stable agent.
 CC 'ST' refers to a heat stable toxin produced by E.coli and other
 CC organisms. Especially the radiostable agent is a therapeutic agent (e.g.
 CC methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive
 CC isotope) or nucleic acid; and the compound is used for the detection,
 CC imaging or treatment of colorectal tumours, particularly metastasised
 CC tumours. The present sequence is a specific example of an ST receptor
 CC binding peptide which can be used in the conjugate
 XX

SQ Sequence 17 AA;

Query Match 94.4%; Score 17; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e-11;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

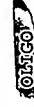
Qy 1 NTFYCCCLCCYPACAGC 17
 Db 1 NTFYCCCLCCYPACAGC 17

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OM protein - protein search, using sw model

Run on: March 26, 2005, 17:12:01 ; Search time 24.4286 Seconds
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Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	1	US-08-141-892A-3
2	18	100.0	18	2	US-08-583-447A-3
3	18	100.0	18	2	US-08-467-920-3
4	18	100.0	18	3	US-08-635-930-3
5	18	100.0	18	3	US-09-193-997-3
6	18	100.0	18	3	US-09-138-237A-3
7	17	94.4	17	1	US-08-141-892A-18
8	17	94.4	17	1	US-08-141-892A-23
9	17	94.4	17	2	US-08-583-447A-18
10	17	94.4	17	2	US-08-583-447A-23
11	17	94.4	17	2	US-08-467-920-18
12	17	94.4	17	2	US-08-467-920-23
13	17	94.4	17	3	US-08-635-930-18
14	17	94.4	17	3	US-08-635-930-23
15	17	94.4	17	3	US-09-193-997-18
16	17	94.4	17	3	US-09-193-997-23
17	17	94.4	17	3	US-09-138-237A-18
18	17	94.4	17	3	US-09-138-237A-23
19	16	88.9	16	1	US-08-141-892A-19
20	16	88.9	16	1	US-08-141-892A-24
21	16	88.9	16	2	US-08-583-447A-19
22	16	88.9	16	2	US-08-583-447A-24
23	16	88.9	16	2	US-08-467-920-19
24	16	88.9	16	2	US-08-467-920-24
25	16	88.9	16	3	US-08-635-930-19
26	16	88.9	16	3	US-08-635-930-24
27	16	88.9	16	3	US-09-193-997-19

28	16	88.9	16	3	US-09-193-997-24	Sequence 24, Appl
29	16	88.9	16	3	US-09-138-237A-19	Sequence 19, Appl
30	16	88.9	16	3	US-09-138-237A-24	Sequence 24, Appl
31	15	83.3	15	1	US-08-141-892A-20	Sequence 20, Appl
32	15	83.3	15	1	US-08-141-892A-25	Sequence 25, Appl
33	15	83.3	15	2	US-08-583-447A-20	Sequence 20, Appl
34	15	83.3	15	2	US-08-583-447A-25	Sequence 25, Appl
35	15	83.3	15	2	US-08-467-920-20	Sequence 20, Appl
36	15	83.3	15	2	US-08-467-920-25	Sequence 25, Appl
37	15	83.3	15	3	US-08-635-930-20	Sequence 20, Appl
38	15	83.3	15	3	US-08-635-930-25	Sequence 25, Appl
39	15	83.3	15	3	US-09-193-997-20	Sequence 20, Appl
40	15	83.3	15	3	US-09-193-997-25	Sequence 25, Appl
41	15	83.3	15	3	US-09-138-237A-20	Sequence 20, Appl
42	15	83.3	15	3	US-09-138-237A-25	Sequence 25, Appl
43	14	77.8	14	1	US-08-141-892A-21	Sequence 21, Appl
44	14	77.8	14	1	US-08-141-892A-26	Sequence 26, Appl
45	14	77.8	14	2	US-08-583-447A-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-141-892A-3
; Sequence 3, Application US/08141892A
; Patent No. 5518888
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
; TITLE OF INVENTION: of Using the Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 55188888ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,892A
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0903
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-141-892A-3

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2,8e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 NTFYCCBLCCYPACAGCN 18
Db 1 NTFYCCBLCCYPACAGCN 18

```
RESULT 2
US-08-583-447A-3
; Sequence 3, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 58796566ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-583-447A-3
Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACACGN 18
Db 1 NTFYCCCLCCYPACACGN 18

RESULT 3
US-08-467-920-3
; Sequence 3, Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WordPerfect 6.0/6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,930
; FILING DATE: 26-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,056
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; ZIP: 19103
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-467-920-3
Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACACGN 18
Db 1 NTFYCCCLCCYPACACGN 18

RESULT 4
US-08-635-930-3
; Sequence 3, Application US/08635930
; Patent No. 6060037
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically Bind To
; TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using
; TITLE OF INVENTION: The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WordPerfect 6.0/6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,930
; FILING DATE: 26-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,056
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; ZIP: 19103
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REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1360
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-635-930-3

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCELCCYPACAGCN 18
Db 1 NTFYCCELCCYPACAGCN 18

RESULT 5
US-09-193-997-3
Sequence 3, Application US/09193997
Patent No. 6087109
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically Bind To Colorectal Cancer Cells
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 6087109ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,997
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,920
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1589
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-193-997-3

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCELCCYPACAGCN 18

Db 1 NTFYCCELCCYPACAGCN 18
RESULT 6
US-09-138-237A-3
Sequence 3, Application US/09138237A
Patent No. 6268159
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: Of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6268159ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,237A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-138-237A-3

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCELCCYPACAGCN 18
Db 1 NTFYCCELCCYPACAGCN 18

RESULT 7
US-08-141-892A-18
Sequence 18, Application US/08141892A
Patent No. 5518888
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: Of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:

;; MEDIUM TYPE: 3.5 inch disk, 720 Kb
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/141,892A
;; FILING DATE: 26-OCT-1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-0903
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-141-892A-18

Query Match 94.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTFYCCELCCYPACAGC 17
Db 1 NTFYCCELCCYPACAGC 17

RESULT 8
US-08-141-892A-23
; Sequence 23, Application US/08141892A
; Patent No. 5518888
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
; TITLE OF INVENTION: of Using the Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888-18
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,892A
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0903
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids

;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-141-892A-23

Query Match 94.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFYCCELCCYPACAGCN 18
Db 1 TFYCCELCCYPACAGCN 17

RESULT 9
US-08-583-447A-18
; Sequence 18, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656-18
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-583-447A-18

Query Match 94.4%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTFYCCELCCYPACAGC 17
Db 1 NTFYCCELCCYPACAGC 17

RESULT 10
US-08-583-447A-23
; Sequence 23, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.

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; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-583-447A-23

Query Match 94.4%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TFYCCELCCYPACACGN 18
Db 1 TFYCCELCCYPACACGN 17

RESULT 11
US-08-467-920-18
; Sequence 18, Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5962220ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FILING DATE:

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-467-920-18

Query Match 94.4%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCELCCYPACAGC 17
Db 1 NTFYCCELCCYPACAGC 17

RESULT 12
US-08-467-920-23
; Sequence 23, Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5962220ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FILING DATE:

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US-08-467-920-23

Query Match 94.4%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFYCCELCCYPACAGCN 18
| | | | | | | | | | | | | | | | | |
Db 1 TFYCCELCCYPACAGCN 17

RESULT 13

US-08-635-930-18
; Sequence 18, Application US/08635930
; Patent No. 6060037

; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically Bind To
; TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using
; TITLE OF INVENTION: The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WordPerfect 6.0/6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,930
; FILING DATE: 26-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,056
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1360
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-635-930-18

Query Match 94.4%; Score 17; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTFYCCELCCYPACAGC 17
| | | | | | | | | | | | | | | | | |
Db 1 NTFYCCELCCYPACAGC 17

RESULT 14

US-08-635-930-23
; Sequence 23, Application US/08635930
; Patent No. 6060037

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically Bind To
; TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using
; TITLE OF INVENTION: The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WordPerfect 6.0/6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,930
; FILING DATE: 26-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,056
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1360
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-635-930-23

Query Match 94.4%; Score 17; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15

US-09-193-997-18
; Sequence 18, Application US/09193997
; Patent No. 6087109

; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESS: No. 6087109ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:


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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/193,997
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/467,920
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-193-997-18

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Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 NTFYCCELCYCYPACAGC 17

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Job time : 24.4286 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2005, 17:25:02 ; Search time 58.1786 Seconds
(without alignments)
102.440 Million cell updates/sec

Title: US-10-775-481A-3

Perfect score: 18

Sequence: 1 NTFYCCBLCYCPACAGCN 18

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	18	10	US-09-930-915A-289
2	18	100.0	18	14	US-10-082-014-79
3	18	100.0	18	14	US-10-372-076-80
4	18	100.0	18	15	US-10-621-684-3
5	18	100.0	18	16	US-10-806-006-289
6	18	100.0	18	16	US-10-677-074-80
7	18	100.0	18	16	US-10-805-913-289
8	18	100.0	18	17	US-10-796-719-3
9	17	94.4	17	15	US-10-621-684-18
10	17	94.4	17	15	US-10-621-684-23
11	16	88.9	16	15	US-10-621-684-19
12	16	88.9	16	15	US-10-621-684-24
13	15	83.3	15	15	US-10-621-684-20

14	15	83.3	15	15	US-10-621-684-25	Sequence 25, Appl
15	15	83.3	18	10	US-09-930-915A-290	Sequence 290, Appl
16	15	83.3	18	14	US-10-082-014-80	Sequence 80, Appl
17	15	83.3	18	14	US-10-372-076-81	Sequence 81, Appl
18	15	83.3	18	16	US-10-806-006-290	Sequence 290, Appl
19	15	83.3	18	16	US-10-677-074-81	Sequence 81, Appl
20	15	83.3	18	16	US-10-805-913-290	Sequence 290, Appl
21	14	77.8	14	14	US-09-930-915A-288	Sequence 288, Appl
22	14	77.8	14	14	US-10-082-014-78	Sequence 78, Appl
23	14	77.8	14	14	US-10-372-076-79	Sequence 79, Appl
24	14	77.8	14	15	US-10-621-684-21	Sequence 21, Appl
25	14	77.8	14	15	US-10-621-684-26	Sequence 26, Appl
26	14	77.8	14	16	US-10-806-006-288	Sequence 288, Appl
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31	10	55.6	17	15	US-10-621-684-8	Sequence 8, Appl
32	10	55.6	17	15	US-10-621-684-41	Sequence 41, Appl
33	10	55.6	18	15	US-10-621-684-7	Sequence 7, Appl
34	10	55.6	18	15	US-10-621-684-13	Sequence 13, Appl
35	10	55.6	18	15	US-10-621-684-38	Sequence 38, Appl
36	10	55.6	18	15	US-10-621-684-39	Sequence 39, Appl
37	10	55.6	18	15	US-10-621-684-40	Sequence 40, Appl
38	10	55.6	18	17	US-10-796-719-2	Sequence 2, Appl
39	10	55.6	18	17	US-10-796-719-4	Sequence 4, Appl
40	10	55.6	18	17	US-10-796-719-11	Sequence 11, Appl
41	10	55.6	19	15	US-10-621-684-2	Sequence 2, Appl
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43	9	50.0	16	15	US-10-621-684-9	Sequence 9, Appl
44	9	50.0	17	15	US-10-621-684-14	Sequence 14, Appl
45	8	44.4	15	15	US-10-621-684-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-930-915A-289
; Sequence 289, Application US/09930915A
; Publication No US20030138769A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED STABILITY
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
; CURRENT APPLICATION NUMBER: US/09/930,915A
; PRIOR FILING DATE: 2001-08-15
; PRIOR FILING DATE: 2000-08-22
; PRIOR FILING DATE: 2000-08-22
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 289
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-930-915A-289

Query Match 100.0%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 4,4e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCBLCYCPACAGCN 18

Db 1 NTFYCCBLCYCPACAGCN 18

RESULT 2

US-10-082-014-79
; Sequence 79, Application US/10082014
; Publication No. US20030185858A1

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; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY
; FILE REFERENCE: ICC-130.0 4564/85124
; CURRENT APPLICATION NUMBER: US/10/082,014
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-082-014-79

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Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 NTFYCCELCCYPACAGCN 18

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; Sequence 80, Application US/10372076
; Publication No. US20030198645A1
; GENERAL INFORMATION:
; APPLICANT: Page, Mark
; APPLICANT: Friede, Martin
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/372,076
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-372-076-80

Query Match      100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NTFYCCELCCYPACAGCN 18
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Db      1 NTFYCCELCCYPACAGCN 18

RESULT 4
US-10-621-684-3
; Sequence 3, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: St Receptor Binding Compounds and
; METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1Iris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA

US-10-621-684-3
; Sequence 3, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY
; FILE REFERENCE: ICC-130.0 4564/85124
; CURRENT APPLICATION NUMBER: US/10/082,014
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn version 3.1
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; LENGTH: 18
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; ORGANISM: Escherichia coli
US-10-082-014-79

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Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 289, Application US/10806006
; Publication No. US20040152876A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; FILE REFERENCE: 4564/91644 ICC-102.2 DV 1
; CURRENT APPLICATION NUMBER: US/10/806,006
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: PCT/US01/41759
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 289
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-806-006-289

Query Match      100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 NTFYCCELCCYPACAGCN 18
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
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; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-621-684-3

Query Match      100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 NTFYCCELCCYPACAGCN 18

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; Publication No. US20040152876A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; FILE REFERENCE: 4564/91644 ICC-102.2 DV 1
; CURRENT APPLICATION NUMBER: US/10/806,006
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: PCT/US01/41759
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
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; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-806-006-289

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Best Local Similarity 100.0%; Pred. No. 4.4e-13;
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; APPLICANT: Page, Mark
; APPLICANT: Friede, Martin
; APPLICANT: Schmidt, Annette Elisabeth
; APPLICANT: Stober, Detlef
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
; TITLE OF INVENTION: CHRONIC HEPATITIS
; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/677,074
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 10/372,076
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-677-074-80

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 NTFYCCCLCCYPACAGCN 18

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US-10-805-913-289
; Sequence 289, Application US/10805913
; Publication No. US20040156864A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; TITLE OF INVENTION: STABILITY
; FILE REFERENCE: 4564/91645 ICC-102.2 DV II
; CURRENT APPLICATION NUMBER: US/10/805,913
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: PCT/US01/41759
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 289
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-805-913-289

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18

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Db 1 NTFYCCCLCCYPACAGCN 18

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; Sequence 3, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-796-719-3

Query Match 100.0%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18

Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 9

US-10-621-684-18
; Sequence 18, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1r18
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229

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; REFERENCE/DOCKET NUMBER: TJU-1702
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-621-684-18
Query Match 94.4%; Score 17; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4e-12; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

Qy 1 NTFYCCCLCCYPACAGC 17
Db 1 NTFYCCCLCCYPACAGC 17

RESULT 10
US-10-621-684-23
; Sequence 23, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-621-684-19
Query Match 88.9%; Score 16; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.5e-11; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

Qy 2 TFYCCCLCCYPACAGC 17
Db 1 TFYCCCLCCYPACAGC 16

RESULT 12
US-10-621-684-24
; Sequence 24, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-621-684-23
Query Match 94.4%; Score 17; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4e-12; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

Qy 2 TFYCCCLCCYPACAGC 18
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;
; COUNTRY: USA
; ZIP: 19103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
;
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-621-684-24
;
; Query Match 88.9%; Score 16; DB 15; Length 16;
; Best Local Similarity 100.0%; Pred. No. 6.5e-11;
; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 3 FYCCELCYPCACGN 18
; Db 1 FYCCELCYPCACGN 16
;
; RESULT 13
; US-10-621-684-20
; Sequence 20, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
;
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
;
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-621-684-25
;
; Query Match 83.3%; Score 15; DB 15; Length 15;
; Best Local Similarity 100.0%; Pred. No. 7.9e-10;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 3 FYCCELCYPCACG 17
; Db 1 FYCCELCYPCACG 15
;
; RESULT 14
; US-10-621-684-25
; Sequence 25, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
;
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
;
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-621-684-25
;
; Query Match 83.3%; Score 15; DB 15; Length 15;
; Best Local Similarity 100.0%; Pred. No. 7.9e-10;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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>

QY 4 YCCELCCTPACGACN 18
 |||||
 Db 1 YCCELCCTPACGACN 15

RESULT 15
 US-09-930-915A-290
 ; Sequence 290, Application US/09930915A
 ; Publication No. US20030138769A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birkett, Ashley J.
 ; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
 ; FILE OF INVENTION: STABILITY
 ; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
 ; CURRENT APPLICATION NUMBER: US/09/930,915A
 ; CURRENT FILING DATE: 2001-08-15
 ; PRIOR APPLICATION NUMBER: 60/226,867
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/225,843
 ; PRIOR FILING DATE: 2000-08-16
 ; NUMBER OF SEQ ID NOS: 313
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 290
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 US-09-930-915A-290

Query Match 83.3%; Score 15; DB 10; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9e-10;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


QY 4 YCCELCCTPACGACN 18
 |||||
 Db 4 YCCELCCTPACGACN 18

Search completed: March 26, 2005, 17:44:31
 Job time : 59.1786 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 17:10:31 ; Search time 18.6429 Seconds
(without alignments)
92.899 Million cell updates/sec

Title: US-10-775-481A-3
Perfect score: 18
Sequence: 1 NTFYCCBLCCYPACAGCN 18
Scoring table:  Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues
Word size : 0
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries

Database : PIR.79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	1 QHEC2	heat-stable entero
2	10	55.6	18	2 A60103	heat-stable entero
3	10	55.6	72	1 QHEC1	heat-stable entero
4	7	38.9	72	1 QHEC4	heat-stable entero
5	7	38.9	72	1 QHEC1B	heat-stable entero
6	6	33.3	53	2 S68705	heat-stable entero
7	6	33.3	66	2 S31652	enterotoxin - Yers
8	6	33.3	71	2 S25659	heat-stable entero
9	6	33.3	90	2 D85845	probable lysis pro
10	6	33.3	534	2 T15414	hypothetical prote
11	6	33.3	862	2 T29133	hypothetical prote
12	6	33.3	924	2 E71476	alanine-tRNA ligas
13	6	33.3	2482	2 I48922	cation-independent
14	6	33.3	2483	1 A49617	insulin-like growt
15	5	27.8	72	2 C39370	rhombotin homolog
16	5	27.8	74	2 AF0925	hypothetical prote
17	5	27.8	75	2 H84631	hypothetical prote
18	5	27.8	80	2 A82531	hypothetical prote
19	5	27.8	108	2 AF1043	hypothetical prote
20	5	27.8	110	2 I74319	gene BHS-2 protein
21	5	27.8	111	2 B72476	hypothetical prote
22	5	27.8	129	2 A24255	chorion class A pr
23	5	27.8	133	2 T17300	hypothetical prote
24	5	27.8	135	2 S34815	nifU protein - Rh
25	5	27.8	156	2 A32795	T-cell translocati
26	5	27.8	187	2 T71464	probable rRNA meth
27	5	27.8	194	2 A83103	conserved hypotet
28	5	27.8	224	2 F81726	conserved hypotet
29	5	27.8	228	2 D95865	probable pentose-5

30	5	27.8	230	2 T20398	hypothetical prote
31	5	27.8	235	2 F70405	hypothetical prote
32	5	27.8	243	2 D85888	hypothetical prote
33	5	27.8	243	2 A91044	hypothetical prote
34	5	27.8	246	2 AG2988	competence protein
35	5	27.8	247	2 AC0923	probable uridine p
36	5	27.8	263	2 G87721	protein ZC123.3 [i
37	5	27.8	265	2 AG0814	cob(II)alamin adeno
38	5	27.8	267	2 B65021	cob(II)alamin adeno
39	5	27.8	275	2 AC0189	probable exported
40	5	27.8	277	1 QOBEC2	HK8FX protein - hu
41	5	27.8	291	2 A99295	competence protein
42	5	27.8	306	2 T24402	hypothetical prote
43	5	27.8	308	2 E90179	hypothetical prote
44	5	27.8	316	1 D71246	hypothetical prote
45	5	27.8	316	2 T49224	SRG1-like protein

ALIGNMENTS

RESULT 1

QHEC2

heat-stable enterotoxin ST-2 - Escherichia coli

C:Species: Escherichia coli

C:Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 09-Jul-2004

C:Accession: A01823

R:Chan, S.K.; Giannella, R.A.

J. Biol. Chem. 256, 7744-7746, 1981

A:Title: Amino acid sequence of heat-stable enterotoxin produced by Escherichia coli pat

A:Reference number: A01823; MUID:81264141; PMID:7021541

A:Accession: A01823

A:Molecule type: protein

A:Residues: 1-18 <CHA>

A:Cross-references: UNIPROT:P01560

A:Experimental source: strain 18D, serotype 0.42:k86:H37

C:Comment: This enterotoxin is one of several, of differing molecular sizes, produced by

idues of the heat-stable enterotoxin ST-1.

C:Superfamily: heat-stable enterotoxin ST

C:Keywords: enterotoxin; heat-stable protein

F:1-18/Product: heat-stable enterotoxin ST-2 #status experimental <MAT>

F:5-10,6-14,9-17/Disulfide bonds: #status predicted

Query Match 100.0%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.7e-15;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCBLCCYPACAGCN 18

Db 1 NTFYCCBLCCYPACAGCN 18

RESULT 2

A60103

heat-stable enterotoxin ST-Ia - Citrobacter freundii

C:Species: Citrobacter freundii

C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004

C:Accession: A60103

R:Guarino, A.; Giannella, R.; Thompson, M.R.

Infect. Immun. 57, 649-652, 1989

A:Title: Citrobacter freundii produces an 18-amino-acid heat-stable enterotoxin identica

A:Reference number: A60103; MUID:89108617; PMID:2912902

A:Accession: A60103

A:Molecule type: protein

A:Residues: 1-18 <GUA>

A:Cross-references: UNIPROT:Q7M0U3

C:Superfamily: heat-stable enterotoxin ST

Query Match 55.6%; Score 10; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e-05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCBLCC 10

```
Db      1 NTFYCCCLCC 10
|||||
RESULT 3
QHEC1
heat-stable enterotoxin ST-I precursor - Escherichia coli
N:Alternate names: heat-stable enterotoxin estA1
C:Species: Escherichia coli
C:Date: 31-Aug-1980 #sequence_revision 31-Aug-1980 #text_change 09-Jul-2004
C:Accession: A01822; A30985; A36732; JT0374; I51932
R:So, M.; McCarthy, B.J.
Proc. Natl. Acad. Sci. U.S.A. 77, 4011-4015, 1980
A:Title: Nucleotide sequence of the bacterial transposon Tn1681 encoding a heat-stable (S)
A:Reference number: A01822; MUID:81054703; PMID:6254008
A:Accession: A01822
A:Molecule type: DNA
A:Residues: 1-72 <LAZ>
A:Cross-references: UNIPROT:P01559; GB:V006612; GB:J01831; NID:G43704; PIDN:CAA23883.1; F
R:Lazure, C.; Seidah, N.G.; Chretien, M.; Lallier, R.; St-Pierre, S.
Can. J. Biochem. Cell Biol. 61, 287-292, 1983
A:Title: Primary structure determination of Escherichia coli heat-stable enterotoxin of
A:Reference number: A30985; MUID:83284515; PMID:6349752
A:Accession: A30985
A:Molecule type: protein
A:Residues: 55-72 <LAZ>
A:Experimental source: strain F11
R:Dallas, W.S.
J. Bacteriol. 172, 5490-5493, 1990
A:Title: The heat-stable toxin I gene from Escherichia coli 18D.
A:Reference number: A36732; MUID:90368614; PMID:2203756
A:Accession: A36732
A:Molecule type: DNA
A:Residues: 1-72 <DAL>
A:Cross-references: GB:M58746; NID:G145860; PIDN:AAA62776.1; PID:G145861
A:Experimental source: strain 18D
R:Stieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.;
Plasmid 20, 42-53, 1988
A:Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escheri
A:Reference number: JT0373; MUID:89202548; PMID:3071819
A:Accession: JT0374
A:Molecule type: DNA
A:Residues: 1-72 <STI>
R:Seikizaki, T.; Akashi, H.; Terakado, N.
Am. J. Vet. Res. 46, 909-912, 1985
A:Title: Nucleotide sequences of the genes for Escherichia coli heat-stable enterotoxin
A:Reference number: I51932; MUID:85249571; PMID:2990268
A:Accession: I51932
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-69, 'P', 71-72 <RES>
A:Cross-references: GB:M25607; NID:G147877; PIDN:AAA24653.1; PID:G147878
C:Comment: Both heat-stable and heat-labile enterotoxins are produced by pathogenic stra
ular sizes.
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-54/Domain: propeptide #status predicted <PRO>
F:55-72/Product: heat-stable enterotoxin ST-I #status experimental <MAT>
F:59-64,60-68,63-71/Disulfide bonds: #status predicted
Query Match 55.6%; Score 10; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 NTFYCCCLCC 10
      . |||||
Db      55 NTFYCCCLCC 64
|||||
RESULT 4
QHEC4
heat-stable enterotoxin STA4 precursor - Escherichia coli
```

```
C:Species: Escherichia coli
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JT0373; A35978
R:Stieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.;
Plasmid 20, 42-53, 1988
A:Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escheri
A:Reference number: JT0373; MUID:89202548; PMID:3071819
A:Accession: JT0373
A:Molecule type: DNA
A:Residues: 1-72 <STI>
A:Cross-references: UNIPROT:P07965; GB:J03311; NID:G147875; PIDN:AAA24652.1; PID:G147876
R:Zhou, X.; Shen, L.P.; Chi, C.W.
Toxicon 28, 453-456, 1990
A:Title: Isolation and nucleotide sequence determination of a gene encoding a heat-stabl
A:Reference number: A35978; MUID:90273381; PMID:2190361
A:Accession: A35978
A:Molecule type: DNA
A:Residues: 1-72 <ZHO>
C:Genetics:
A:Gene: estA4
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-53/Domain: propeptide #status predicted <PRO>
F:54-72/Product: heat-stable enterotoxin #status predicted <MAT>
F:59-64,60-68,63-71/Disulfide bonds: #status predicted
Query Match 38.9%; Score 7; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4 YCCCLCC 10
      . |||||
Db      58 YCCCLCC 64
|||||
RESULT 5
QHEC1B
heat-stable enterotoxin ST-Ib precursor - Escherichia coli
N:Alternate names: heat-stable enterotoxin ST-A2
C:Species: Escherichia coli
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C:Accession: JS0292; A33068; A33067; A30567
R:Moseley, S.L.; Hardy, J.W.; Hug, M.I.; Echeverria, P.; Falkow, S.
Infect. Immun. 39, 1167-1174, 1983
A:Title: Isolation and nucleotide determination of a gene encoding a heat-stable enteroto
A:Reference number: JS0292; MUID:83184648; PMID:6341230
A:Accession: JS0292
A:Molecule type: DNA
A:Residues: 1-72 <MOS>
A:Cross-references: UNIPROT:Q47185; UNIPROT:P07965; GB:M34916; NID:G146407; PIDN:AAA2399(C
R:Dwarakanath, P.; Visweswariah, S.S.; Subrahmanyam, Y.V.B.K.; Shanthi, G.; Jagannatha,
Gene 81, 219-226, 1989
A:Title: Cloning and hyperexpression of a gene encoding the heat-stable toxin of Escheri
A:Reference number: A33068; MUID:90034194; PMID:2680769
A:Accession: A33068
A:Molecule type: DNA
A:Residues: 1-18, 'A', 20-72 <DWA>
A:Cross-references: GB:M23255; NID:G148029; PIDN:AAA24686.1; PID:G148030
R:Aimoto, S.; Takao, T.; Shimonishi, Y.; Hara, S.; Takeda, T.; Takeda, Y.; Miwatani, T.
Eur. J. Biochem. 129, 257-263, 1982
A:Title: Amino acid sequence of heat-stable enterotoxin produced by human enterotoxigenic
A:Reference number: A33067; MUID:83105138; PMID:6759126
A:Accession: A33067
A:Molecule type: protein
A:Residues: 54-72 <AIM>
R:Guzman-Verduzco, L.M.; Kupersztovich, Y.M.
Infect. Immun. 57, 645-648, 1989
A:Title: Rectification of two Escherichia coli heat-stable enterotoxin allele sequences
A:Reference number: A30567; MUID:89108616; PMID:2643580
A:Accession: A30567
A:Molecule type: DNA
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A;Residues: 1-18,'A',20-24,'AG',27-41,'V',43-44,'N',46,'E',48,'S',50-72 <GUZ>
A;Cross-references: GB:M18345; NID:g145862; PIDN:AAA23729.1; PID:g145863
C;Comment: This is one of the type I heat-stable enterotoxins that are methanol-soluble.
C;Genetics:
A;Gene: st
C;Superfamily: heat-stable enterotoxin ST
C;Keywords: enterotoxin; heat-stable protein
F;1-53/Domain: signal sequence and propeptide #status predicted <SIG>
F;54-72/Product: heat-stable enterotoxin ST-1b #status experimental <MAT>
F;59-64,60-68,63-71/Disulfide bonds: #status experimental

Query Match 38.9%; Score 7; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0

Qy 4 YCCCLCC 10
Db 58 YCCCLCC 64

RESULT 6
S68705
heat-stable enterotoxin Y-STC - Yersinia enterocolitica
C;Species: Yersinia enterocolitica
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: S68705
R;Yoshino, K.; Takao, T.; Huang, X.; Murata, H.; Nakao, H.; Takeda, T.; Shimonishi, Y.
FEBS Lett. 362, 319-322, 1995
A;Title: Characterization of a highly toxic, large molecular size heat-stable enterotoxin
A;Reference number: S68705; MUID:95246844; PMID:7729521
A;Accession: S68705
A;Molecule type: protein
A;Residues: 1-53 <YOS>
A;Experimental source: strain 86-11
C;Superfamily: heat-stable enterotoxin ST
C;Keywords: enterotoxin; heat-stable protein
F;41-46,42-50,45-53/Disulfide bonds: #status predicted

Query Match 33.3%; Score 6; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.7; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0

Qy 5 CCECLCC 10
Db 41 CCECLCC 46

RESULT 7
S31652
enterotoxin - Yersinia kristensenii
C;Species: Yersinia kristensenii
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S31652
R;Ibrahim, A.; Liesack, W.; Stackebrandt, E.
submitted to the EMBL Data Library, November 1992
A;Reference number: S31652
A;Accession: S31652
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-56 <IBR>
A;Cross-references: UNIPROT:P31518; EMBL:X69218; NID:g48617; PIDN:CAA49152.1; PID:g48618
C;Superfamily: heat-stable enterotoxin ST

Query Match 33.3%; Score 6; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0

Qy 12 PACAGC 17
Db 61 PACAGC 66

RESULT 8
S25659
heat-stable enterotoxin yst precursor - Yersinia enterocolitica
C;Species: Yersinia enterocolitica
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S25659; A41474; A23114; S65849
R;Ibrahim, A.; Liesack, W.; Pike, S.; Stackebrandt, E.
FEMS Microbiol. Lett. 97, 63-66, 1992
A;Title: The polymerase chain reaction: an epidemiological tool to differentiate between
A;Reference number: S25659
A;Accession: S25659
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-71 <IBR>
A;Cross-references: UNIPROT:P07593; EMBL:X65999; NID:g48611; PIDN:CAA46801.1; PID:g48612
R;Delor, I.; Kaeckenbeeck, A.; Wauters, G.; Cornelis, G.R.
Infect. Immun. 58, 2983-2988, 1990
A;Title: Nucleotide sequence of yst, the Yersinia enterocolitica gene encoding the heat-
A;Reference number: A41474; MUID:90354067; PMID:2201642
A;Accession: A41474
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-47,'S',49-71
A;Cross-references: GB:U09235; NID:g487394; PIDN:AAA18472.1; PID:g487395
R;Takao, T.; Tominaga, N.; Yoshimura, S.; Shimonishi, Y.; Hara, S.; Inoue, T.; Miyama, A.
Eur. J. Biochem. 152, 199-206, 1985
A;Title: Isolation, primary structure and synthesis of heat-stable enterotoxin produced
A;Reference number: A23114; MUID:86004705; PMID:4043080
A;Accession: A23114
A;Molecule type: protein
A;Residues: 54-71 <YAK>
R;Mikulskis, A.V.; Delor, I.; Ha Thi, V.; Cornelis, G.R.
Mol. Microbiol. 14, 905-915, 1994
A;Title: Regulation of the Yersinia enterocolitica enterotoxin yst gene. Influence of gr
A;Reference number: S65849; MUID:95231297; PMID:7715452
A;Accession: S65849
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-43 <MIK>
A;Cross-references: EMBL:U09235
C;Genetics:
A;Gene: yst
C;Superfamily: heat-stable enterotoxin ST
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-41/Domain: propeptide #status predicted <PRO>
F;42-71/Product: heat-stable enterotoxin yst #status predicted <MAT>

Query Match 33.3%; Score 6; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 2; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0

Qy 12 PACAGC 17
Db 66 PACAGC 71

RESULT 9
D85845
probable lysis protein S of prophage CP-933V Z3340 [imported] - Escherichia coli (strain
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D85845
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimantanta, E.; Potamouis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: D85845
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <STO>
A;Cross-references: UNIPROT:Q8X4M8; GB:AE005174; NID:g12516391; PIDN:AGS7224.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:

A;Gene: Z3340

Query Match 33.3%; Score 6; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FYCCCL 8

DB 7 FYCCCL 12

RESULT 10

T15414

hypothetical protein C05E11.4 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T15414

R;Geisel, C.

submitted to the EMBL Data Library, April 1996

A;Description: The sequence of *C. elegans* cosmid C05E11.

A;Reference number: Z18347

A;Accession: T15414

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-534 <GEI>

A;Cross-references: UNIPROT:P54145; EMBL:U53338; NID:g1255840; PID:g1255843; PIDN:AAA961

A;Experimental source: strain Bristol N2; clone C05E11

C;Genetics:

A;Gene: CESP:C05E11.4

A;Map position: X

A;Introns: 43/1; 151/1; 182/3; 229/3; 339/2; 394/3; 423/3; 490/1

C;Superfamily: ammonium transport protein amt1

Query Match

Best Local Similarity 33.3%; Score 6; DB 2; Length 534;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ACACGN 18

DB 307 ACACGN 312

RESULT 11

T29133

hypothetical protein SCIF2.24 - *Streptomyces coelicolor* (fragment)

C;Species: *Streptomyces coelicolor*

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C;Accession: T29133

R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1998

A;Reference number: Z17215

A;Accession: T29133

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-862 <PAR>

A;Cross-references: UNIPROT:Q8CJM2; EMBL:AL031350; NID:e1316892; PID:e1316916; PIDN:CAA2

C;Genetics:

A;Note: SCIF2.24

Query Match

Best Local Similarity 33.3%; Score 6; DB 2; Length 862;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YPACAG 16

DB 397 YPACAG 402

RESULT 12

E71476

alanine-tRNA ligase (EC 6.1.1.7) - *Chlamydia trachomatis* (serotype D, strain UW3/Cx)

C;Species: *Chlamydia trachomatis*

C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 17-Mar-2003

C;Accession: E71476
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: *Chlamydia trachomatis*
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: E71476
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-924 <ARN>
A;Cross-references: GB:AE001346; GB:AE001273; NID:g3329203; PIDN:AAC68344.1; PID:g3329203
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:

A;Gene: alas

C;Superfamily: alanyl-tRNA ligase

C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 33.3%; Score 6; DB 2; Length 924;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FYCCCL 8

DB 39 FYCCCL 44

RESULT 13

I48922

cation-independent mannose 6-phosphate/insulin-like growth factor II receptor precursor

C;Species: *Mus musculus* (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999

C;Accession: I48922

R;Ludwig, T.; Tenschler, K.; Remmler, J.; Hoflack, B.; Lobel, P.

Gene 142, 311-312, 1994

A;Title: Cloning and sequencing of cDNAs encoding the full length mouse mannose 6-phosphate

A;Reference number: I48922; MUID:94252588; PMID:8194771

A;Accession: I48922

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-2482 <RES>

A;Cross-references: EMBL:U04710; NID:g451552; PIDN:AAA19568.1; PID:g451553

C;Superfamily: mannose 6-phosphate receptor, cation-independent; fibronectin type II repeat

C;Keywords: growth factor receptor

F:1895-1934/Domain: fibronectin type II repeat homology <2F1>

Query Match

Best Local Similarity 33.3%; Score 6; DB 2; Length 2482;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YPACAG 16

DB 2177 YPACAG 2182

RESULT 14

A49617

insulin-like growth factor II / cation-independent mannose 6-phosphate receptor precursor

C;Species: *Mus musculus* (house mouse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: A49617; B39538; A48700; A46439; I52815; I65739; A57529

R;Szebenyi, G.; Rotwein, P.

Genomics 19, 120-129, 1994

A;Title: The mouse insulin-like growth factor II/cation-independent mannose 6-phosphate

A;Reference number: A49617; MUID:94245146; PMID:8188212

A;Accession: A49617

A;Molecule type: DNA

A;Residues: 1-2483 <SZE>

A;Cross-references: UNIPROT:Q07113; GB:I22143; NID:g431410; PIDN:AAA39320.1; PID:g431412

R;Szebenyi, G.; Rotwein, P.

J. Biol. Chem. 266, 5534-5539, 1991

A;Title: Differential regulation of mannose 6-phosphate receptors and their ligands durin

A;Reference number: A39538; MUID:91170218; PMID:1848553

A;Accession: B39538

A;Molecule type: DNA

A:Residues: 435-488 <SZ2>
A:Cross-references: GB:M58586
R:Chen, H.J.; Remmler, J.; Delaney, J.C.; Messner, D.J.; Lobel, P.
J. Biol. Chem. 268, 22338-22346, 1993
A:Title: Mutational analysis of the cation-independent mannose 6-phosphate/insulin-like
is important for intracellular targeting of lysosomal enzymes.
A:Reference number: A48700; MUID:94042390; PMID:8226743
A:Accession: A48700
A:Molecule type: mRNA
A:Residues: 2249-2483 <CHE>
A:Cross-references: GB:L19500; NID:g407325; PIDN:AAA16037.1; PID:g407326
R:Stoeger, R.; Kubicka, P.; Liu, C.G.; Kafri, T.; Razin, A.; Cedar, H.; Barlow, D.P.
Cell 73, 61-71, 1993
A:Title: Maternal-specific methylation of the imprinted mouse Igf2r locus identifies the
A:Reference number: A46439; MUID:93214996; PMID:8462104
A:Accession: A46439
A:Molecule type: DNA
A:Residues: 1-44 <STO>
A:Cross-references: GB:L06445; NID:g293379; PIDN:AAA37921.1; PID:g553942
A:Note: sequence extracted from NCBI backbone (NCBIN:128531, NCBI:P:128532)
R:Stoeger, R.; Kubicka, P.; Liu, C.
Cell 73, 1-11, 1993
A:Title: Maternal-specific methylation of the imprinted mouse Igf2r locus identifies the
A:Reference number: 152815; MUID:93214982; PMID:8462093
A:Accession: 152815
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-44 <RES>
A:Cross-references: GB:L06445; NID:g293379; PIDN:AAA37921.1; PID:g553942
A:Accession: 155739
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 93-106 <RE2>
A:Cross-references: GB:L06446; NID:g293381; PIDN:AAA37922.1; PID:g293382
R:Liu, Z.; Mitranc, D.W.; Kim, S.; Rotwein, P.
Mol. Endocrinol. 9, 1477-1487, 1995
A:Title: Control of insulin-like growth factor-II/mannose 6-phosphate receptor gene tran
A:Reference number: A57529; MUID:96130821; PMID:8584025
A:Accession: A57529
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-44 <LIU>
A:Cross-references: GB:U26348; NID:g973191; PIDN:AAA98844.1; PID:g973192
C:Genetics:
A:Gene: Igf2r
C:Function: <LYSO>
A:Description: transports lysosomal enzymes marked by the presence of mannose 6-phosphat
C:Function: <IGFR>
A:Description: binds to, internalizes, and may play a role in transmembrane signalling c
C:Superfamily: mannose 6-phosphate receptor, cation-independent; fibronectin type II rep
C:Keywords: duplication; growth factor receptor; transmembrane protein
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-2294/Domain: extracellular #status predicted <EXT>
F:1896-1935/Domain: fibronectin type II repeat homology <2F1>
F:2295-2316/Domain: transmembrane #status predicted <TMW>
F:2317-2483/Domain: intracellular #status predicted <INT>

Query Match 33.3%; Score 6; DB 1; Length 2483;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 YPACAG 16
| | | | |
Db 2178 YPACAG 2183

RESULT 15
C39370
rhombotin homolog 3 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 15-Mar-2004
C:Accession: C39370
R:Boehm, T.; Foroni, L.; Kaneko, Y.; Perutz, M.F.; Rabbitts, T.H.

Proc. Natl. Acad. Sci. U.S.A. 88, 4367-4371, 1991
A:Title: The rhombotin family of cysteine-rich LIM-domain oncogenes: distinct members ar
A:Reference number: A39370; MUID:91239569; PMID:2034676
A:Accession: C39370
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-72 <BOE>
A:Cross-references: GB:M64358
C:Genetics:
A:Gene: GDB:LMO3; RBTN2
A:Cross-references: GDB:127816; OMIM:180386
A:Map position: 12p13-12p13
F:16-69/Domain: LIM metal-binding repeat homology <LIM2>

Query Match 27.8%; Score 5; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CAGCN 18
| | | | |
Db 16 CAGCN 20

Search completed: March 26, 2005, 17:25:59
Job time : 18.6429 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	166.5	30.4	115	2	US-07-903-029-5	Sequence 5, Appli
2	163.5	29.8	115	2	US-07-903-029-4	Sequence 4, Appli
3	135	24.6	115	2	US-07-903-029-6	Sequence 6, Appli
4	81	14.8	15	1	US-08-145-940-2	Sequence 1, Appli
5	81	14.8	16	1	US-08-145-940-1	Sequence 2, Appli
6	81	14.8	16	2	US-08-583-447A-56	Sequence 56, Appli
7	78	14.2	15	2	US-08-583-447A-55	Sequence 55, Appli
8	69.5	12.7	1940	2	US-08-644-271-30	Sequence 30, Appli
9	69.5	12.7	1940	4	US-09-077-955-34	Sequence 34, Appli
10	68.5	12.5	221	3	US-08-896-933-29	Sequence 29, Appli
11	68.5	12.5	221	3	US-09-314-235-29	Sequence 29, Appli
12	68.5	12.5	221	4	US-09-708-008B-29	Sequence 29, Appli
13	67.5	12.3	251	3	US-09-144-778B-16	Sequence 16, Appli
14	67.5	12.3	251	4	US-08-882-431B-16	Sequence 16, Appli
15	67	12.2	770	1	US-08-525-654A-1	Sequence 1, Appli
16	67	12.2	771	1	US-08-525-654A-3	Sequence 3, Appli
17	66.5	12.1	218	4	US-09-893-737-28	Sequence 28, Appli
18	66.5	12.1	719	4	US-09-949-016-7766	Sequence 7766, Ap
19	66	12.0	655	4	US-09-328-352-6455	Sequence 6455, Ap
20	64.5	11.8	503	4	US-09-252-991A-22790	Sequence 22790, A
21	64	11.7	211	4	US-09-540-236-2321	Sequence 2321, A
22	64	11.7	700	4	US-09-902-540-14225	Sequence 14225, A
23	64	11.7	917	2	US-08-588-983-16	Sequence 16, Appli
24	64	11.7	917	2	US-08-588-976-16	Sequence 16, Appli
25	63.5	11.6	498	1	US-08-357-598-9	Sequence 9, Appli
26	63.5	11.6	498	2	US-09-003-289-9	Sequence 9, Appli
27	63.5	11.6	498	5	PCR-US95-16435-9	Sequence 9, Appli


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; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-145-940-2

Query Match 14.8%; Score 81; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 0.002;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 93 DECELCINVACTGC 106
DB 1 DDCELCNVACTGC 14

RESULT 5
US-08-145-940-1
; Sequence 1, Application US/08145940
; Patent No. 5489670
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Kita, Toehiro
; APPLICANT: Smith, Christine E.
; APPLICANT: Fok, Kam F.
; TITLE OF INVENTION: Human Uroguanylin
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,940
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: 07-21(808)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; MOLECULE TYPE: linear
US-08-145-940-1

Query Match 14.8%; Score 81; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 0.002;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 93 DECELCINVACTGC 106
DB 2 DDCELCNVACTGC 15

RESULT 6
US-08-583-447A-56
; Sequence 56, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
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; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-583-447A-55

Query Match 14.2%; Score 78; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 0.0046;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 DECELCINVACTGC 106
Db 2 EDCELCINVACTGC 15

RESULT 8
US-08-644-271-30
; Sequence 30, Application US/08644271
; Patent No. 5814478
; GENERAL INFORMATION:
; APPLICANT: Valenzuela, et al.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS
; AND LIGANDS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/644,271
; FILING DATE: 10-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/008,657
; FILING DATE: 15-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 195A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; TELEX:
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1940 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; FEATURE:
; NAME/KEY: Rat Agrin
; LOCATION: 1...1940
; OTHER INFORMATION:
; US-08-644-271-30

Query Match 12.7%; Score 69.5; DB 2; Length 1940;
Best Local Similarity 26.2%; Pred. No. 39;
Matches 21; Conservative 7; Mismatches 19; Indels 33; Gaps 3;

Qy 49 DPQQKSGLLPDVCYNPALDLDPVCASQEAASFTFKALRTIATDECEL-----97
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Qy 98 -----CINVACT 104
Db 130 RLLRQGPCGSRDPCANVTCS 149

RESULT 9
US-09-077-955-34
; Sequence 34, Application US/09077955A
; Patent No. 6413740
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al., David M.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
; FILE REFERENCE: REG195-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/077,955A
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PCT/US96/20696
; EARLIER FILING DATE: 1996-12-13
; EARLIER APPLICATION NUMBER: 08/644,271
; EARLIER FILING DATE: 1996-05-10
; EARLIER APPLICATION NUMBER: 60/008,657
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 34
; LENGTH: 1940
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-09-077-955-34

Query Match 12.7%; Score 69.5; DB 4; Length 1940;
Best Local Similarity 26.2%; Pred. No. 39;
Matches 21; Conservative 7; Mismatches 19; Indels 33; Gaps 3;

Qy 49 DPQQKSGLLPDVCYNPALDLDPVCASQEAASFTFKALRTIATDECEL-----97
Db 79 EPSVEDPGRASCVCCKNACPATVAVCGSD--ASTY-----SNECELQRAQCNCQORRI 129
Qy 98 -----CINVACT 104
Db 130 RLLRQGPCGSRDPCANVTCS 149

RESULT 10
US-08-896-933-29
; Sequence 29, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
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; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-896-933-29

Query Match      12.5%; Score 68.5; DB 3; Length 221;
Best Local Similarity 24.5%; Pred. No. 2.7; 29; Indels 35; Gaps 4;
Matches 26; Conservative 16; Mismatches 29; Indels 35; Gaps 4;

Qy 15 VLQSAQGVYIKYHGFQVQLSVKLNLEEKQMSDPQOKSGLLPDCVYNPALPL--DLQ 72
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Db 14 LVKNLQNIYFLYEGDPVTHENVKSDQL-----LSHDLIYVSGPNYDKLK 59

Qy 73 PVCASQEAATFKALRTIATDE-----CELCINVACTGC 106
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 60 TELKNQEMATLTK-----DKNVDIYGVYHYHLCYLCAERSAC 98

RESULT 11
US-09-314-235-29
; Sequence 29, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-29

Query Match      12.5%; Score 68.5; DB 3; Length 221;
Best Local Similarity 24.5%; Pred. No. 2.7;
Matches 26; Conservative 16; Mismatches 29; Indels 35; Gaps 4;

Qy 15 VLQSAQGVYIKYHGFQVQLSVKLNLEEKQMSDPQOKSGLLPDCVYNPALPL--DLQ 72
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Db 14 LVKNLQNIYFLYEGDPVTHENVKSDQL-----LSHDLIYVSGPNYDKLK 59

Qy 73 PVCASQEAATFKALRTIATDE-----CELCINVACTGC 106
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 60 TELKNQEMATLTK-----DKNVDIYGVYHYHLCYLCAERSAC 98

RESULT 12
US-09-708-008B-29
; Sequence 29, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; PRIOR APPLICATION NUMBER: 07/891,718
; PRIOR FILING DATE: 1992-06-01
; PRIOR APPLICATION NUMBER: US91/00342
; PRIOR FILING DATE: 1991-01-17
; PRIOR APPLICATION NUMBER: 07/466,577
; PRIOR FILING DATE: 1990-01-17
; PRIOR APPLICATION NUMBER: 07/416,530
; PRIOR FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-708-008B-29

Query Match      12.5%; Score 68.5; DB 4; Length 221;
Best Local Similarity 24.5%; Pred. No. 2.7;
Matches 26; Conservative 16; Mismatches 29; Indels 35; Gaps 4;

Qy 15 VLQSAQGVYIKYHGFQVQLSVKLNLEEKQMSDPQOKSGLLPDCVYNPALPL--DLQ 72
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 14 LVKNLQNIYFLYEGDPVTHENVKSDQL-----LSHDLIYVSGPNYDKLK 59

Qy 73 PVCASQEAATFKALRTIATDE-----CELCINVACTGC 106
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 60 TELKNQEMATLTK-----DKNVDIYGVYHYHLCYLCAERSAC 98

RESULT 13
US-09-144-776B-16
; Sequence 16, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-144-776B-16

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RESULT 15

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2005, 16:48:40 ; Search time 105.613 Seconds
(without alignments)
332.314 Million cell updates/sec

Title: US-10-775-481A-55

Perfect score: 548

Sequence: 1 MSGQLWAAVLLLVLSQA.....LRTIATDECELCINVACTGC 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*

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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*

17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*

18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*

19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	356	65.0	112	17	US-10-479-606-5
2	252.5	46.1	109	17	US-10-479-606-6
3	166.5	30.4	115	9	US-09-981-353-61
4	166.5	30.4	115	14	US-10-235-994-22
5	166.5	30.4	115	14	US-10-262-473-12
6	166.5	30.4	115	17	US-10-479-606-4
7	120	21.9	102	14	US-10-262-473-14
8	120	21.9	108	14	US-10-262-473-16
9	97.5	17.8	87	9	US-09-925-299-1162
10	97.5	17.8	87	10	US-09-925-299-1162
11	84	15.3	16	14	US-10-107-814-20
12	84	15.3	85	9	US-09-925-299-1527
13	84	15.3	85	10	US-09-925-299-1527

14	81	14.8	16	14	US-10-107-814-1	Sequence 1, Appli
15	81	14.8	16	14	US-10-197-954-141	Sequence 141, App
16	81	14.8	16	15	US-10-621-684-56	Sequence 56, Appl
17	81	14.8	16	17	US-10-479-606-2	Sequence 2, Appli
18	81	14.8	16	17	US-10-760-085-141	Sequence 141, App
19	78	14.2	14	14	US-10-107-814-21	Sequence 21, Appl
20	78	14.2	15	15	US-10-621-684-55	Sequence 55, Appl
21	75	13.7	169	16	US-10-437-963-156045	Sequence 156045,
22	73.5	13.4	402	16	US-10-437-963-132955	Sequence 132955,
23	70.5	12.9	242	15	US-10-424-599-275208	Sequence 275208,
24	69.5	12.7	458	15	US-10-369-493-17284	Sequence 17284, A
25	69.5	12.7	742	16	US-10-437-963-185159	Sequence 185159,
26	69.5	12.7	1937	15	US-10-072-012-792	Sequence 792, App
27	69.5	12.7	1940	13	US-10-016-283-34	Sequence 34, Appl
28	69.5	12.7	1940	15	US-10-072-012-791	Sequence 791, App
29	69.5	12.7	1959	15	US-10-072-012-790	Sequence 790, App
30	69	12.6	15	17	US-10-479-606-3	Sequence 3, Appli
31	69	12.6	866	16	US-10-437-963-183310	Sequence 183310,
32	68.5	12.5	358	15	US-10-335-977-6075	Sequence 6075, Ap
33	68.5	12.5	431	15	US-10-276-774-1563	Sequence 1563, Ap
34	68.5	12.5	547	8	US-08-834-705-2	Sequence 2, Appli
35	68.5	12.5	547	15	US-10-282-122A-59002	Sequence 59002, A
36	68.5	12.5	549	15	US-10-335-977-6076	Sequence 6076, Ap
37	68.5	12.5	549	15	US-10-335-977-6077	Sequence 6077, Ap
38	68	12.4	72	17	US-10-796-719-21	Sequence 21, Appl
39	68	12.4	220	14	US-10-002-784A-26	Sequence 26, Appl
40	68	12.4	235	16	US-10-437-963-203716	Sequence 203716,
41	68	12.4	468	14	US-10-002-784A-27	Sequence 27, Appl
42	68	12.4	900	16	US-10-437-963-105276	Sequence 105276,
43	67.5	12.3	251	8	US-08-882-431-16	Sequence 16, Appl
44	67.5	12.3	251	14	US-10-002-784A-16	Sequence 16, Appl
45	67.5	12.3	1074	15	US-10-389-566-2371	Sequence 2371, Ap

ALIGNMENTS

RESULT 1

US-10-479-606-5

; Sequence 5, Application US/10479606

; Publication No. US20050032684A1

; GENERAL INFORMATION:

; APPLICANT: Cetin, Yalcin

; TITLE OF INVENTION: Guanylate-cyclase C ligand, administered via the airways, for the

; TITLE OF INVENTION: treatment of respiratory airway problems

; FILE REFERENCE: 03100192aa

; CURRENT APPLICATION NUMBER: US/10/479.606

; PRIOR FILING DATE: 2003-12-04

; PRIOR APPLICATION NUMBER: DE10127119.0

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: PCT/DE02/02040

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 5

; LENGTH: 112

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-479-606-5

Query Match 65.0%; Score 356; DB 17; Length 112;
Best Local Similarity 65.7%; Pred. No. 1.5e+33;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

Qy ...2 SGSQLWAAVLLLVLSQAQGVYKYHGFQVLESVKKLEEKQMSDPQOKSGLLPDV 61

Db 7 SGLPGVAVVLLLVLSQAQGVYKYHGFQVLESVKKLEEKQMSDPQOKSGLLPDV 66

Qy 62 CYNPALPDLQPCVCAQEAATFKALRTIATDECELCINVACTGC 106

Db 67 CHHPALPDLQPCVCAQEAATFKALRTIATDECELCINVACTGC 111


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Query Match 30.4%; Score 166.5; DB 14; Length 115;
Best Local Similarity 35.1%; Pred. No. 2.3e-11;
Matches 40; Conservative 15; Mismatches 32; Indels 27; Gaps 4;

QY 7 WAAVLLLVLSAQGVYIKYHGFGVQLSVKLNLEEKQMSDPQOQKSG-----56
DB 15 WAAL-----AGGVTVDGNGFSLSPRVGKLNRFAPIPG 61
QY 57 --LLPDVCYNPALPLDLPVCASQEAASFTFKALRTIATD--ECELINVACTGC 106
DB 62 BPVVFILCSNPFPPEELPKCKEPNAQEIQLRLEIEADPGTCEICAVAACTGC 115

RESULT 6
US-10-479-606-4
; Sequence 4, Application US/10479606
; Publication No. US20050032684A1
; GENERAL INFORMATION:
; APPLICANT: Cetin, Yalcin
; APPLICANT: Savas, Yukeel
; TITLE OF INVENTION: Guanylate-cyclase C ligand, administered via the airways, for the
; FILE OF INVENTION: treatment of respiratory airway problems
; CURRENT APPLICATION NUMBER: US/10/479,606
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: DE10127119.0
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/DE02/02040
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 115
; TYPE: PRT
; ORGANISM: rat or homo sapiens (guanylin)
; US-10-479-606-4

Query Match 30.4%; Score 166.5; DB 17; Length 115;
Best Local Similarity 35.1%; Pred. No. 2.3e-11;
Matches 40; Conservative 15; Mismatches 32; Indels 27; Gaps 4;

QY 7 WAAVLLLVLSAQGVYIKYHGFGVQLSVKLNLEEKQMSDPQOQKSG-----56
DB 15 WAAL-----AGGVTVDGNGFSLSPRVGKLNRFAPIPG 61
QY 57 --LLPDVCYNPALPLDLPVCASQEAASFTFKALRTIATD--ECELINVACTGC 106
DB 62 BPVVFILCSNPFPPEELPKCKEPNAQEIQLRLEIEADPGTCEICAVAACTGC 115

RESULT 7
US-10-262-473-14
; Sequence 14, Application US/10262473
; Publication No. US20030199442A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John,
; APPLICANT: Burgess, Catherine,
; APPLICANT: Gorman, Linda,
; APPLICANT: Guo, Xiaojia,
; APPLICANT: Lepley, Denise,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rastelli, Luca,
; APPLICANT: Reiger, Daniel,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-462B
; CURRENT APPLICATION NUMBER: US/10/262,473
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-262-473-16

Query Match 21.9%; Score 120; DB 14; Length 108;
Best Local Similarity 33.0%; Pred. No. 5.9e-06;
Matches 34; Conservative 12; Mismatches 39; Indels 18; Gaps 5;

QY 7 WAAVLLLVLSAQGVYIKYHGFGVQLSVKLNLEEKQMSDPQOQKSGLLPDVCYNP 65
DB 18 WAAL-----AGGVTVDGNGFSLSPRVGKLNRFAPIP-GEF-----VVPILCSNP 62
QY 66 ALPLDLQPVCSAQEAASFTFKALRTIATD--ECELINVACTGC 106
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; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 14
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-262-473-14

Query Match 21.9%; Score 120; DB 14; Length 102;
Best Local Similarity 33.0%; Pred. No. 5.5e-06;
Matches 34; Conservative 12; Mismatches 39; Indels 18; Gaps 5;

QY 7 WAAVLLLVLSAQGVYIKYHGFGVQLSVKLNLEEKQMSDPQOQKSGLLPDVCYNP 65
DB 15 WAAL-----AGGVTVDGNGFSLSPRVGKLNRFAPIP-GEF-----VVPILCSNP 59
QY 66 ALPLDLQPVCSAQEAASFTFKALRTIATD--ECELINVACTGC 106
DB 60 NFPEELPKCKEPNAQEIQLRLEIEADPGTCEICAVAACTGC 102

RESULT 8
US-10-262-473-16
; Sequence 16, Application US/10262473
; Publication No. US20030199442A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John,
; APPLICANT: Burgess, Catherine,
; APPLICANT: Gorman, Linda,
; APPLICANT: Guo, Xiaojia,
; APPLICANT: Lepley, Denise,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rastelli, Luca,
; APPLICANT: Reiger, Daniel,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-462B
; CURRENT APPLICATION NUMBER: US/10/262,473
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-262-473-16

Query Match 21.9%; Score 120; DB 14; Length 108;
Best Local Similarity 33.0%; Pred. No. 5.9e-06;
Matches 34; Conservative 12; Mismatches 39; Indels 18; Gaps 5;

QY 7 WAAVLLLVLSAQGVYIKYHGFGVQLSVKLNLEEKQMSDPQOQKSGLLPDVCYNP 65
DB 18 WAAL-----AGGVTVDGNGFSLSPRVGKLNRFAPIP-GEF-----VVPILCSNP 62
QY 66 ALPLDLQPVCSAQEAASFTFKALRTIATD--ECELINVACTGC 106
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db 63 NFPEELKPLCKEPNPAOEILORLEEIAEDPPTCEICAYAACTGC 105

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RESULT 9
; Sequence 1162, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1162
; LENGTH: 87

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: TYPE: PRT
: ORGANISM: Homo sapiens
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: FEATURE:
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: NAME/KEY: SITE
: LOCATION: (60)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
:
: NAME/KEY: SITE
: LOCATION: (61)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
:
: NAME/KEY: SITE
: LOCATION: (70)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
:
: NAME/KEY: SITE
: LOCATION: (80)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
:
: US-09-925-299-1162

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Query Match 17.8%; Score 97.5; DB 9; Length 87;
Best Local Similarity 29.1%; Pred. No. 0.0019;
Matches 23; Conservative 13; Mismatches 28; Indels 15; Gaps 2;

QY 43 EEKQNSDPQQOKSG-----LLPDVCYNPALPLDLQPVCASQEAASTFKALRTI 90
| | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Dh 9 EIKDIQEPORGVCKIRNFAPITGPEVVPITICSNPNFEEELPKPICKSPNRRXXEGRWKS 68

Qy 91 ATDECELINV---ACTGC 106
| : : ||||
pb 69 LXDPGHMKSVXTLACTGC 87

RESULT 10
US-09-925-299-1162
; Sequence 1162, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1162

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;
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

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? NAME/KEY: SITE
? LOCATION: (60)
? OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
?
? NAME/KEY: SITE
? LOCATION: (61)
? OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
?
? NAME/KEY: SITE
? LOCATION: (70)
? OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
?
? NAME/KEY: SITE
? LOCATION: (80)
? OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
?
? US-09-925-299-1162

```

Query Match 17.8%; Score 97.5; DB 10; Length 87;
Best Local Similarity 29.1%; Pred. No. 0.0019;
Matches 23; Conservative 13; Mismatches 28; Indels 15; Gaps 2;

Qy 91 ATDECELCINV---ACTGC 106
pb 69 LXPDPGHMKSVXTLACTGC 87

```

RESULT 11
US-10-107-814-20
; Sequence 20, Application US/10107814
; Publication No. US20030073628A1
; GENERAL INFORMATION:
; APPLICANT: SHAILUJHAI, KUNWAR
; APPLICANT: NIKIFOROVICH, GREGORY
; APPLICANT: JACOB, GARY S.
; TITLE OF INVENTION: GUANYLATE CYCLIC
; TITLE OF INVENTION: OF TISSUE INFL
; FILE REFERENCE: 81361/284943/MAS
; CURRENT APPLICATION NUMBER: US/10/1
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20

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1 / LENGTH: 16
2 / TYPE: PRT
3 / ORGANISM: Artificial Sequence
4 /
5 / FEATURE:
6 / OTHER INFORMATION: Description of Artificial Sequence: Synthetic
7 /
8 / OTHER INFORMATION: guanylate cyclase receptor agonist peptide
9 /
10 / NAME/KEY: DISULFID
11 / LOCATION: (4) ..(12)
12 / NAME/KEY: DISULFID
13 / LOCATION: (7) ..(15)
14 /
15 / DIS-10-107-814-20

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Query Match 15.3%; Score 84; DB 14; Length 16;
Best Local Similarity 92.9%; Pred. No. 0.0079;
Matches 13: Conservative 1; Mismatches 0; Indels 0; Gaps 0

Qy 93 DECELCIN VACTGC 106
|||||:|||||
Db 2 DECELCIN VACTGC 15

RESULT 12
US-09-925-299-1527
; Sequence 1527, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299


```
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1527
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (28)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (31)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (32)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (34)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (38)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (39)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (42)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (43)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (47)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (52)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (53)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (55)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (66)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (70)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
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; LOCATION: (71)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (83)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1527
Query Match 15.3%; Score 84; DB 9; Length 85;
Best Local Similarity 33.8%; Pred. No. 0.07;
Matches 23; Conservative 10; Mismatches 35; Indels 0; Gaps 0;
QY 2 SCSQLWAARVLLLVLOSAGVYIKYHGFQVLESVKKLNELEEKQMSDPQOKSGILLPDV 61
DB 17 SGLTGLAEVLXLXLTQXGXQYXXFRVXLESXXLXDLXAWAPSPXLEAXXLAARV 76
QY 62 CYNPALPL 69
DB 77 CHHPALXL 84
RESULT 13
US-09-925-299-1527
; Sequence 1527, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1527
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (28)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (29)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (31)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (32)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (34)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (38)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (39)
```

```

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (42)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (43)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (47)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (52)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (53)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (55)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (66)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (70)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (71)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (83)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-925-299-1527

```

Query Match	15.3%;	Score 84;	DB 10;	Length 85;
Best Local Similarity	33.8%;	Pred.No. 0.07;		
Matches 23; Conservative	10;	Mismatches 35;	Indels 0;	Gaps 0;
QY	2	SGSQLWAVLLLVLSAQGVYIKYHGFVQLSEVKLNLEEKQMSDPQQOKSGLLPDV	61	
		: : : : : : : : : :		
Dd	17	SGLLTGLAEVLXXLXTXQGXQYXXFRVKLESMMXLXDLEAXWSPLEXAXLLAAV	76	
QY	62	CYNPALPL	69	
		::::		
Dd	77	CHHPALXL	84	

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RESULT 14
US-10-107-814-1
; Sequence 1, Application US/10107814
; Publication No. US20030073628A1
; GENERAL INFORMATION:
; APPLICANT: SHAILUBHAI, KUNWAR
; APPLICANT: NIKIFOROVICH, GREGORY
; APPLICANT: JACOB, GARY S.
; TITLE OF INVENTION: GUANYLATE CYCLASE RECEPTOR AGONISTS FOR THE TREATMENT
; OF TISSUE INFLAMMATION AND CARCINOGENESIS
; FILE REFERENCE: 81361/284943/MAS
; CURRENT APPLICATION NUMBER: US/10/107,814
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (4) .. (12)
; NAME/KEY: DISULFID
; LOCATION: (7) .. (15)

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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:37:49 ; Search time 22.438 Seconds
(without alignments)
454.541 Million cell updates/sec

Title: US-10-775-481A-55
Perfect score: 548
Sequence: 1 MSGSQLMAVLLLVLSQAQ.....LRTIATDECELCINVACTGC 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	356	65.0	112	JC4651	uroguanylin precursor
2	167.5	30.6	116	JC7620	guanylin precursor
3	166.5	30.4	115	A46279	Guanylin precursor
4	135	24.6	115	JN0318	guanylin precursor
5	134.5	24.5	116	B46279	guanylin precursor
6	74	13.5	354	JQ0413	alkanal monooxygen
7	73	13.3	189	S2521	coatomer protein z
8	72.5	13.2	228	S45677	proteinase inhibitor
9	70.5	12.9	72	QHEC18	heat-stable entero
10	70.5	12.9	368	A82249	response regulator
11	69.5	12.7	236	S18786	exotoxin type A pr
12	69.5	12.7	458	B83912	NADP-specific glut
13	69.5	12.7	824	I50618	c-fps proto oncoge
14	69.5	12.7	1959	AGRT	agrin - rat
15	68.5	12.5	236	S18783	exotoxin type A pr
16	68.5	12.5	251	S29659	exotoxin type A pr
17	68.5	12.5	342	AC3027	hypothetical prote
18	68.5	12.5	342	G98257	tetrahydropteroylt
19	68.5	12.5	547	B64701	probable 60K inner
20	68.5	12.5	549	E71818	probable inner mem
21	68	12.4	72	QHEC4	heat-stable entero
22	68	12.4	533	T1906	protein-tyrosine k
23	67.5	12.3	1074	T01906	hypothetical prote
24	67	12.2	873	B33225	ecdysone-induced p
25	67	12.2	1210	A48001	phospholipase C (E
26	66.5	12.1	357	B84678	hypothetical prote
27	66.5	12.1	462	I61730	lamina associated
28	66.5	12.1	873	TVFVFS	protein-tyrosine k
29	66	12.0	183	A49313	microfibril-associ

30	66	12.0	406	2	T23277	hypothetical prote
31	66	12.0	1259	2	T32901	hypothetical prote
32	65	11.9	235	2	G72501	hypothetical prote
33	65	11.9	247	2	B83708	phosphonates trans
34	65	11.9	274	2	E91185	probable ATP-bind
35	65	11.9	274	2	C86032	probable ATP-bind
36	65	11.9	274	2	S47791	hypothetical prote
37	65	11.9	496	2	D83614	conserved hypothet
38	64.5	11.8	495	2	D83167	leucine aminopepti
39	64.5	11.8	711	1	S28391	protein-tyrosine-p
40	64.5	11.8	711	2	T45160	protein-tyrosine-p
41	64	11.7	445	2	T72251	hypothetical prote
42	64	11.7	799	2	H70832	carbon-monoxide de
43	64	11.7	852	2	T46091	hypothetical prote
44	64	11.7	917	1	S15885	hexokinase (EC 2.7
45	64	11.7	993	2	E71392	ATP-dependent RNA

ALIGNMENTS

RESULT 1

JC4651
uroguanylin precursor - human
N:Alternate names: Guanylyl cyclase activating peptide II
C:Species: Homo sapiens (man)
C:Date: 10-May-1996 #sequence revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: JC4651; S63702; S68052
R:Miyazato, M.; Nakazato, M.; Yamaguchi, H.; Date, Y.; Kojima, M.; Kangawa, K.; Matsuo, Biochem. Biophys. Res. Commun. 219, 644-648, 1996
A:Title: Cloning and characterization of a cDNA encoding a precursor for human uroguanylin
A:Reference number: JC4651; MUID:96193705; PMID:8605041
A:Accession: JC4651
A:Molecule type: mRNA
A:Residues: 1-112 <MUY>
A:Cross-references: UNIPROT:Q16661; GB:U34279; NID:gl236798; PIDN:AAC50416.1; PID:gl2367
R:Hill, O.; Cetin, Y.; Cieslak, A.; Maegert, H.J.; Forssmann, W.G.
Biochim. Biophys. Acta 1253, 146-149, 1995
A:Title: A new human guanylate cyclase-activating peptide (GCAP-II, uroguanylin): precu
A:Reference number: S63702; MUID:96106424; PMID:8519795
A:Accession: S63702
A:Molecule type: mRNA
A:Residues: 1-112 <HML>
A:Cross-references: EMBL:Z50753; NID:g974823; PIDN:CAA90629.1; PID:g974824
R:Hess, R.; Kuhn, M.; Schulz-Knappe, P.; Raida, M.; Fuchs, M.; Klodt, J.; Adermann, K.;
FEBS Lett. 374, 34-38, 1995
A:Title: GCAP-II: isolation and characterization of the circulating form of human urogu
A:Reference number: S68052; MUID:96049550; PMID:7589507
A:Accession: S68052
A:Molecule type: protein
A:Residues: 89-99,'X',101-102,'X',104-107,'X',109-110,'X',112 <HES>
C:Comment: This protein, a member of the guanylin peptide family, is an endogenous activ

Query Match 65.0%; Score 356; DB 2; Length 112;
Best Local Similarity 65.7%; Pred. No. 9.8e-30;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

Qy 2 SGSQLMAVLLLVLSQAQGVYIKYHGFVQLSEVKLNLEEKQMSDPQOQKSGLLPDV 61

Db 7 SGLPGVAVLLLLQLQTSQVYIQGFRVQLSEMKKLSLEAQWAPSRLQASLLPAV 66

Qy 62 CYNPALPLDQPCVCAQEAASATFKALRTIATDECELCINVACTGC 106

Db 67 CHHPALPDQLQPCVCAQEAASISFKLTITANDDCELCVNVACTGC 111

RESULT 2

JC7620
guanylin precursor, long form - European eel
C;Species: Anguilla anguilla (European eel)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
R;Comrie, M.M.; Cutler, C.P.; Cramb, G.
Biochem. Biophys. Res. Commun. 281, 1078-1085, 2001
A;Title: Cloning and expression of guanylin from the European eel (*Anguilla anguilla*).
A;Reference number: JC7620; MUID:21139737; PMID:11243845
A;Accession: JC7620
A;Molecule type: mRNA
A;Residues: 1-116 <COM>
A;Cross-references: GB:A3701673
C;Comment: This protein, a member of a family of heat-stable peptides, is a potent extra-
cellular signalling system plays a role in osmoregulation in euryhaline teleost
fish.
C;Superfamily: guanylin
C;Keywords: heat-stable protein; osmoregulation
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-116/Product: guanylin precursor, long form #status predicted <MAT>
F;33-39/Region: homologous #status predicted
F;69-114/Region: highly conserved #status predicted

Query Match 30.6%; Score 167.5; DB 2; Length 116;
Best Local Similarity 41.9%; Pred. No. 3.6e-10;
Matches 44; Conservative 10; Mismatches 44; Indels 7; Gaps 4;

QY 8 AAVLLILAV---LQSAQGVYIKYHGFQVLESVKKLE-LEEKQMSDPQOKSGLLPDVCY 63
Db 12 AVLLILAFVLCEREGASALFNRLVDITPPDCEICANAACTGC 70

QY 64 NPALPLDLPVCASQEAATFKALRTIAT--DECELCINVACTGC 106
Db 71 NPHLPARFLVCRREGASALFNRLVDITPPDCEICANAACTGC 115

RESULT 3
A46279
guanylin precursor [validated] - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: A46279; S29228; S29807
R;de Sauvage, F.J.; Keshav, S.; Kuang, W.J.; Gillett, N.; Henzel, W.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 89, 9089-9093, 1992
A;Title: Precursor structure, expression, and tissue distribution of human guanylin.
A;Reference number: A46279; MUID:93028409; PMID:1409606
A;Accession: A46279
A;Molecule type: mRNA
A;Residues: 1-115 <DE1>
A;Cross-references: UNIPROT:Q02747; GB:M95174; NID:G306823; PIDN:AAA58625.1; PID:G306824
A;Note: sequence extracted from NCBI backbone (NCBIN:115377, NCBIPI:115378)
R;Wiegand, R.C.; Kato, J.; Huang, M.D.; Fok, K.F.; Kachur, J.F.; Currie, M.G.
FEBS Lett. 311, 150-154, 1992
A;Title: Human guanylin: cDNA isolation, structure, and activity.
A;Reference number: S29228; MUID:93011964; PMID:1327879
A;Accession: S29228
A;Molecule type: mRNA
A;Residues: 1-115 <WIE>
A;Cross-references: GB:M97496; NID:G183414; PIDN:AAA35915.1; PID:G183415
R;Kuhn, M.; Raide, M.; Adermann, K.; Schulz-Knappe, P.; Gerzer, R.; Heim, J.M.; Forssman
FEBS Lett. 318, 205-209, 1993
A;Title: The circulating bioactive form of human guanylin is a high molecular weight pep
A;Reference number: S29807; MUID:93178628; PMID:8095028
A;Accession: S29807
A;Molecule type: protein
A;Residues: 22-68 <KUH>
A;Experimental source: plasma
C;Comment: amino-terminal sequencing of mature form and molecular weight of mature form by
n of the same receptor.
A;Gene: GDB:GUCA2
A;Cross-references: GDB:I36460; OMIM:139392
A;Map position: lp35-lp34

C;Superfamily: guanylin
C;Keywords: hormone; intestine
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-115/Product: guanylin #status experimental <MAT>

Query Match 30.4%; Score 166.5; DB 1; Length 115;
Best Local Similarity 35.1%; Pred. No. 4.5e-10;
Matches 40; Conservative 15; Mismatches 32; Indels 27; Gaps 4;

QY 7 WAAVLLLVLSQAQGVYIKYHGFQVLESVKKLELEEKQMSDPQOKSG----- 56
Db 15 WAAAL-----AGVTVDGNGFSLSVKXKLDLQ-----PQPRVKLRNFAPIPG 61

QY 57 --LLPDVCYNPALPLDLPVCASQEAATFKALRTIAT--DECELCINVACTGC 106
Db 62 EPVVPILCSNPFPBELKPLCKEPNAQEILQRLLEEIAEDPGTCEICAYAACTGC 115

RESULT 4
JN0318
guanylin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Dec-1992 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JN0318; A43345; A38184; S25489
R;Wiegand, R.C.; Kato, J.; Currie, M.G.
Biochem. Biophys. Res. Commun. 185, 812-817, 1992
A;Title: Rat guanylin cDNA: characterization of the precursor of an endogenous activator
A;Reference number: JN0318; MUID:92328783; PMID:1378267
A;Accession: JN0318
A;Molecule type: mRNA
A;Residues: 1-115 <WIE>
A;Cross-references: UNIPROT:P28902; GB:M93005; NID:G204540; PIDN:AAA41300.1; PID:G204541
R;Schulz, S.; Christman, T.D.; Garbers, D.L.
J. Biol. Chem. 267, 16019-16021, 1992
A;Title: Cloning and expression of guanylin. Its existence in various mammalian tissues.
A;Reference number: A43345; MUID:92355545; PMID:1379587
A;Accession: A43345
A;Molecule type: mRNA
A;Residues: 1-115 <SCH>
A;Cross-references: GB:M95493; NID:G204542; PIDN:AAA41302.1; PID:G204543
A;Experimental source: intestine
A;Note: sequence extracted from NCBI backbone (NCBIN:110474, NCBIPI:110476)
R;Currie, M.G.; Fok, K.F.; Kato, J.; Moore, R.J.; Hamra, F.K.; Duffin, K.L.; Smith, C.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 947-951, 1992
A;Title: Guanylin: an endogenous activator of intestinal guanylate cyclase.
A;Reference number: A38184; MUID:92141235; PMID:1346555
A;Accession: A38184
A;Molecule type: protein
A;Residues: 101-115 <CUR>
A;Experimental source: jejunum
A;Note: sequence extracted from NCBI backbone (NCBIPI:79480)
R;Maegert, H.J.; Khun, M.; Kruhoffer, M.; Forssmann, W.G.
submitted to the EMBL Data Library, August 1992
A;Reference number: S25489
A;Accession: S25489
A;Molecule type: mRNA
A;Residues: 101-115 <MAE>
A;Cross-references: EMBL:X67669; NID:G56343; PIDN:CAA47901.1; PID:G56344
C;Comment: Guanylin is an endogenous ligand for an intestine-specific receptor guanylyl
n of the same receptor.
C;Superfamily: guanylin
C;Keywords: hormone; intestine
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-115/Product: guanylin #status predicted <MAT>

Query Match 24.6%; Score 135; DB 1; Length 115;
Best Local Similarity 33.0%; Pred. No. 8.3e-07;
Matches 37; Conservative 12; Mismatches 51; Indels 12; Gaps 3;

QY 7 WAAVLLLVLSQAQGVYIKYHGFQVLESVKKLELEEKQMSDPQOKSGLL----- 58
Db 4 WLLSVLCLLGLALVLVEGVTVQDGLSPFLSVKQLKHLREVQETLMSHKKFAFLRLPKP 63

[illegible]

```
Db 1 MSSLSLYTVOAVLLDQOGERIYAKYQPPHRSDGHHQVSKVQKQFEKQLYRKH 60
QY 53 QKSGLL--PD--VCYNPALPLDLPVCASQE-----AASFFKALR 88
Db 61 QDSELIIFEDHLVLYKEYIDITIVLVASLENEIVLOGFSAIR 104
RESULT 8
S45677
A:Molecule type: mRNA
A:Residues: 1-228 <JOH>
A:Cross-references: UNIPROT:Q26057; EMBL:X79512; NID:g498784; PIDN:CAA56043.1; PID:g4987
A:Keywords: serine proteinase inhibitor
F:21-66/Domain: Kazal proteinase inhibitor
F:72-119/Domain: Kazal proteinase inhibitor homology <KP1>
F:123-170/Domain: Kazal proteinase inhibitor homology <KP2>
F:174-221/Domain: Kazal proteinase inhibitor homology <KP4>
Query Match 13.2%; Score 72.5; DB 2; Length 228;
Best Local Similarity 27.3%; Pred. No. 5.2;
Matches 33; Conservative 13; Mismatches 42; Indels 33; Gaps 6;
QY 7 WAAVALLLVLSAQ-----GVVIKYGQVQLE-----SVKKLNELEEK 45
Db 8 WITTLVAVASTARCPSCPLNPKVCGSLDLYGNSCQLNAICNPSLKL--YDGP 65
QY 46 QMSDPQKSGLLPDVVCYNPALPLDLPVCASQ-EAASFFKALRTIATDECELCINVACT 104
Db 66 CIDKPOQ-----PLDYNFVCGTDGKTYNLCALRIACNPNHLNLRVDYQ 116
QY 105 G 105
Db 117 G 117
RESULT 9
QHECIB
A:Alternate names: heat-stable enterotoxin - Escherichia coli
A:Species: Escherichia coli
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
R:Accession: J0292; A33068; A33067; A30567
R:Moseley, S.L.; Hardy, J.W.; Huq, M.I.; Echeverria, P.; Falkow, S.
Infect. Immun. 39, 1167-1174, 1983
A:Title: Isolation and nucleotide determination of a gene encoding a heat-stable enterotoxin
A:Reference number: J0292; MUID:83184648; PMID:6341230
A:Accession: J0292
A:Molecule type: DNA
A:Residues: 1-72 <MOS>
A:Cross-references: UNIPROT:Q47185; UNIPROT:P07965; GB:M34916; NID:g146407; PIDN:AAA2399
R:Dwarkanath, P.; Visweswariah, S.S.; Subrahmanyam, Y.V.B.K.; Shanthi, G.; Jagannatha,
Gene 81, 219-226, 1989
A:Title: Cloning and hyperexpression of a gene encoding the heat-stable toxin of Escherichia coli
A:Reference number: A33068; MUID:90034194; PMID:2680769
A:Accession: A33068
A:Molecule type: DNA
A:Residues: 1-18, 'A', 20-72 <DNA>
A:Cross-references: GB:M29255; NID:g148029; PIDN:AAA24686.1; PID:g148030
A:Note: the authors translated the codon AAG for residue 2 as Val and CTA for residue 34
R:Aimoto, S.; Takao, T.; Shimonishi, Y.; Hara, S.; Takeda, Y.; Miwatani, T.
Eur. J. Biochem. 129, 257-263, 1982
A:Title: Amino acid sequence of heat-stable enterotoxin produced by human enterotoxigenic
A:Reference number: A33067; MUID:83105138; PMID:6759126
A:Accession: A33067
```

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A:Molecule type: protein
A:Residues: 54-72 <AIM>
R:Guzman-Verduzco, L.M.; Kupersztosch, Y.M.
Infect. Immun. 57, 645-648, 1989
A:Title: Rectification of two Escherichia coli heat-stable enterotoxin allele sequences
A:Reference number: A30567; MUID:89108616; PMID:2643580
A:Accession: A30567
A:Molecule type: DNA
A:Residues: 1-18, 'A', 20-24, 'AG', 27-41, 'V', 43-44, 'N', 46, 'E', 48, 'S', 50-72 <GUZ>
A:Cross-references: GB:M18345; NID:g145862; PIDN:AAA23729.1; PID:g145863
C:Comment: This is one of the type I heat-stable enterotoxins that are methanol-soluble.
C:Genetics:
A:Gene: st
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:1-53/Domain: signal sequence and propeptide #status predicted <SIG>
F:54-72/Product: heat-stable enterotoxin ST-Ib #status experimental <MAT>
F:59-64,60-68,63-71/Disulfide bonds: #status experimental
Query Match 12.9%; Score 70.5; DB 1; Length 72;
Best Local Similarity 32.8%; Pred. No. 2.5;
Matches 19; Conservative 6; Mismatches 18; Indels 15; Gaps 2;
QY 63 YNPALPLDLPVCASQEAASFFKALRTIATDE-----CELCINVACTGC 106
Db 15 FSP-PPQDAKPVESSKEKITLEKKNTAKSKNGSPESMNSNYCCCLCCNPACTGC 71
RESULT 10
A82249
A:Alternate names: response regulator VC1050 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
A:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
R:Accession: A82249
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: A82249
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-368 <HEI>
A:Cross-references: UNIPROT:Q9KT55; GB:AE004186; GB:AE003852; NID:g9655507; PIDN:AAF94203
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1050
A:Map position: 1
C:Superfamily: response regulator, Hnr type; response regulator homology
Query Match 12.9%; Score 70.5; DB 2; Length 368;
Best Local Similarity 30.7%; Pred. No. 14;
Matches 31; Conservative 21; Mismatches 30; Indels 19; Gaps 6;
QY 4 SOLWAAVLLLV-----LQSAQGVYIKYHGQV-----QLESVKKLNELEEK---QMS 48
Db 19 AQITAAKLILLVDDPFRRTKQ-YLQYGTQVIEAENGLDGLKRLDHPDLILCOLS 77
QY 49 DPQOKSGLLPDVVCYN-PALPLDLPVCASQEAASFFKALR 88
Db 78 MPVLNGIEFVEEVSSVPSPLPLV--VSATEMADVAKALR 116
RESULT 11
S18786
A:Alternate names: A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isolate
X:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes phage
A:Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain N
isolate United Kingdom; strain MGAS496 isolate Germany
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C:Accession: S18786; S18787; S18788; S18790; S18792; S18795; S18799
```

```

RESULT 12
E83912
NADP-specific glutamate dehydrogenase gdhA [imported] - Bacillus halodurans (strain C-12)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: E83912
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: E83912
A>Status: preliminary
A:Molecule type: DNA
A:Cross-references: UNIPROT:Q9KB34; GB:AP001514; GB:BA000004; NID:gi0174613; PIDN:BA8058
A:Experimental source: strain C-125
C:Genetics:
A:Gene: gdhA
C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 12.7%; Score 69.5; DB 2; Length 458;
Best Local Similarity 32.6%; Pred. No. 22;
Matches 30; Conservative 15; Mismatches 22; Indels 25; Gaps 6;

Qy 5 QLVAAVLLLVLSQAQGYIKYHGFQVLESVKKLENEEEKQMSD-----PQ-----QOKS 55
Db 264 QLGAKV----VACSDSGGV-YDKNGIDLTQVKLKEVERKRISYVNEHPHAHYVGCS 318

Qy 56 GLLPDCVYNPALPLDLQPVCAQ-----EAAST 83
Db 319 GIW-----SVPCDIALPCATQNELDEAAAT 343

RESULT 13
I50618
C-fps proto oncogene - chicken
C:Species: Gallus gallus (Chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50618
R:Huang, C.C.; Hammond, C.; Bishop, J.M.
J. Mol. Biol. 181, 175-186, 1985
A:Title: Nucleotide sequence and topography of chicken c-fps. Genesis of a retroviral on
A:Reference number: I50618; MUID:85160839; PMID:3879969
A:Accession: I50618
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-824 <HUA>
A:Cross-references: UNIPROT:Q90778; EMBL:X02266; NID:g63203; PIDN:CAA26155.1; PID:g87104
C:Genetics:
A:Gene: C-fps
A:Introns: 75/3; 133/3; 166/1; 227/2; 273/2; 313/2; 354/2; 416/3; 442/3; 512/3; 553/3; 5
C:Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology
C:Keywords: ATP
F:462-547/Domain: SH2 homology <SH2>
F:561-823/Domain: protein kinase homology <KIN>
F:569-577/Region: protein kinase ATP-binding motif

Query Match 12.7%; Score 69.5; DB 2; Length 824;
Best Local Similarity 27.8%; Pred. No. 41;
Matches 25; Conservative 17; Mismatches 25; Indels 23; Gaps 4;

Qy 24 IKYHGFQVLESVKKLENEEKQ-MSDPQOKSGLL-----PDVCYN----- 64
Db 340 VELRGEELASPGERVHLLKRGLOEAQQQLGLVCAQAKLQAEQDMLANKLAEIGSEE 399

Qy 65 --PALPL--DLQPVCAQSEAASTFKALRTI 90
Db 400 PPPALPLQEDRQSCVSTQERSGVTALETI 429

RESULT 14
AGRT
Agrin - rat

```


GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:37:18 ; Search time 91.2993 Seconds
(without alignments)
594.533 Million cell updates/sec

Title: US-10-775-481A-55

Perfect score: 548

Sequence: 1 MSGSQLWAVLLLLVLSAQ.....LRTIATDELCINACTGC 106

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	100.0	106	1	GUAAU RAT
2	500.5	91.3	107	2	Q8R5G8
3	500	91.2	106	1	GUAAU MOUSE
4	500	91.2	106	2	Q9QU03
5	356	65.0	112	1	GUAAU HUMAN
6	335	61.1	111	1	GUAAU CAVEPO
7	311	56.8	113	1	GUAAU PIG
8	278.5	50.8	109	1	GUAAU DIDMA
9	174.5	31.8	109	1	GUAAU PIG
10	167.5	30.6	108	2	Q98T10
11	167.5	30.6	108	2	Q7ZS20
12	167.5	30.6	116	2	Q98T19
13	166.5	30.4	115	1	GUAAU HUMAN
14	150.5	27.5	110	2	Q7ZS21
15	149	27.2	107	1	GUAAU CAVEPO
16	142	25.9	109	2	Q7ZS22
17	137	25.0	115	2	Q8R5G9
18	135	24.6	115	1	GUAAU RAT
19	134.5	24.5	116	1	GUAAU MOUSE
20	99	18.1	119	2	Q70674
21	75	13.7	61	2	Q6VEG8
22	74	13.5	354	1	LXAL PHOLE
23	73.5	13.4	346	2	Q943F0
24	73.5	13.4	397	2	Q8S255
25	73	13.3	189	1	COPE2 YEAST
26	73	13.3	254	2	Q6VFN9
27	73	13.3	1139	1	M2A2 HUMAN
28	72.5	13.2	228	2	Q26057
29	72	13.1	800	2	Q6DRN3
30	71	13.0	268	2	Q7S0G1
31	71	13.0	713	2	Q6L968

32 71 13.0 775 2 Q72HT2 thermus the
33 70.5 12.9 368 2 Q9KT55 Q9455 vibrio chol
34 70.5 12.9 710 2 Q949U6 Q949u6 arabidopsis
35 70.5 12.9 710 2 Q8H1E8 Q8h1e8 arabidopsis
36 70.5 12.9 751 2 Q9LUU0 Q9luu0 arabidopsis
37 70 12.8 72 1 HST2_ECOLI Q47185 escherichia
38 70 12.8 274 2 Q8ZL88 Q8z188 salmonella
39 70 12.8 793 2 Q8IBJ8 Q8ibj8 plasmodium
40 69.5 12.7 236 2 Q57453 Q57453 streptococ
41 69.5 12.7 300 2 Q9RC89 Q9rc89 bacillus ha
42 69.5 12.7 458 2 Q9KB34 Q9kb34 bacillus ha
43 69.5 12.7 610 2 Q8CM38 Q8cm38 streptococ
44 69.5 12.7 639 2 Q8ESL4 Q8esl4 streptococ
45 69.5 12.7 824 2 Q90778 Q90778 gallus galli

ALIGNMENTS

RESULT 1

GUAAU RAT
ID GUAAU RAT STANDARD; PRT; 106 AA.
AC P70658;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Uroguanylin precursor (UGN) (Guanylate cyclase activator 2B).
GN Name=Guca2b;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 92-106.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97248740; PubMed=9094754; DOI=10.1016/S0167-0115(96)02103-9;
RA Li Z., Perkins A.G., Peters M.F., Campa M.J., Goy M.F.;
RT "Purification, cDNA sequence, and tissue distribution of rat uroguanylin";
RL Regul. Pept. 68:45-56(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97131589; PubMed=8977100; DOI=10.1016/S0014-5793(96)01235-5;
RA Miyazato M., Nakazato M., Matsukura S., Kangawa K., Matsuo H.;
RT "Uroguanylin gene expression in the alimentary tract and extra-gastrointestinal tissues";
RL FEBS Lett. 398:170-174(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Small intestine;
RX MEDLINE=97319300; PubMed=9176203;
RA Blanchard R.K., Cousins R.J.;
RT "Upregulation of rat intestinal uroguanylin mRNA by dietary zinc restriction";
RL Am. J. Physiol. 272:G972-G978(1997).

CC -1- FUNCTION: Endogenous activator of intestinal guanylate cyclase. It stimulates this enzyme through the same receptor binding region as the heat-stable enterotoxins. May be a potent physiological regulator of intestinal fluid and electrolyte transport. May be an autocrine/paracrine regulator of intestinal salt and water transport.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed not only in the gastrointestinal tract but also in the lung, pancreas and kidney.

CC -1- SIMILARITY: Belongs to the guanylin family.

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RN Nature 420:563-573 (2002).
RN [8]
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=2049374; PubMed=1042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [9]
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20530913; PubMed=1076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [10]
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Kidney;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai Y., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai T.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toyota T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBSJ databases.
DR ENBL; AF006668; AAD09311.1; -.
DR ENBL; BC024373; AAH24373.1; -.
DR ENBL; U67800; AAD02215.1; -.
DR ENBL; AK002364; BAB22042.1; -.
DR HSSP; Q16661; IUYA.
DR GO; MGI:1270851; Guca2b.
DR GO; GO:0005615; Cytoplasmic space; TAS.
DR GO; GO:0006182; P:GMP biosynthesis; IMP.
DR GO; GO:0047789; P:fluid secretion; IMP.
DR GO; GO:0045716; P:negative regulation of blood pressure; IMP.
DR InterPro; IPR000879; Guanylin.
DR Pfam; PF02058; Guanylin; 1.
DR PIRSF; PIRSF001849; Guanylin; 1.
DR PRINTS; PR00774; GUANYLIN.
DR ProDom; PD005586; Guanylin; 1.
SQ SEQUENCE 106 AA; 11627 MW; 30FF1CCB59D293DA8 CRC64;
Query Match 91.2%; Score 500; DB 2; Length 106;
Best Local Similarity 90.6%; Pred. No. 3,9e-43;
Matches 96; Conservative 7; Mismatches 3; Indels 0; Gaps 0
Qy 1 MSGSQLWAAVLLLVLSQAQGVYIKYHGFVQLSEVKQMLEBPKQMSDPQOQSGLLPD 60
Db 1 MRSQSQLWAAVLLLVLSQAQGVYIKYHGFVQLSEVKQMLEBPKQMSDPQOQSGLLPD 60
Qy 61 VCNPALPLDLPVCASQEAASFTKALRTIATDECELGINVACTGC 106
Db 61 VCNPALPLDLPVCASQEAASFTKALRTIATDECELGINVACTGC 106
RESULT 5
GUAU HUMAN STANDARD; PRT; 112 AA.
AC Q16661;

```


CC autocrine/paracrine regulator of intestinal salt and water
 CC transport.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the guanylin family.
 CC -----
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 CC -----
 DR EMBL; Z74738; CAA98994.1; -.
 DR HSPF; Q16661; IUYA.
 DR InterPro; IPR000879; Guanylin.
 DR Pfam; PF02058; Guanylin; 1.
 DR PIRSF; PIRSF001849; Guanylin; 1.
 DR PRINTS; PR00774; GUANYLIN.
 DR ProDom; PD005588; Guanylin; 1.
 KW SIGNAL.
 FT SIGNAL 1 26 Potential.
 FT PROPEP 27 96
 FT PEPTIDE 97 111 Uroguanylin.
 FT DISULFID 67 80 Potential.
 FT DISULFID 100 108 By similarity.
 FT DISULFID 103 111 By similarity.
 SQ SEQUENCE 111 AA; 12125 MW; 7C3366A721FE0411 CRC64;
 Query Match 61.1%; Score 335; DB 1; Length 111;
 Best Local Similarity 65.3%; Pred. No. 2.8e-26;
 Matches 64; Conservative 13; Mismatches 21; Indels 0; Gaps 0;
 QY 9 AVLLLLVLSAQGVYIKYGHFQVLESVKKLEELBEKQMSDPQOKSGLLPDVCYNPALP 68
 Db 14 AVILLLLQGTQSDIKYQGVLESVKKLEELBEKQMSDPQOKSGLLPDVCYNPALP 73
 QY 69 LDLPQVCASQAASSTFKALRTIATDECELCINACTGC 106
 Db 74 LDLPQICTSQAASITLQALRTMDNDECELCVNIATGTC 111
 RESULT 7
 GUAY_PIG ID GUAY_PIG STANDARD; PRT; 113 AA.
 AC O13009;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Uroguanylin precursor (UGN) (Guanylate cyclase activator 2B)
 DE (Guanylate cyclase C activating peptide II) (GCAP-II).
 GN Name-GUCA2B;
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Jejunum;
 RA Hill O., Maegert H.J., Forssmann W.-G.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Endogenous activator of intestinal guanylate cyclase. It
 CC stimulates this enzyme through the same receptor binding region as
 CC the heat-stable enterotoxins. May be a potent physiological
 CC regulator of intestinal fluid and electrolyte transport. May be an
 CC autocrine/paracrine regulator of intestinal salt and water
 CC transport (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- SIMILARITY: Belongs to the guanylin family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z83746; CAB06042.1; -.
 DR HSPF; Q16661; IUYA.
 DR InterPro; IPR000879; Guanylin.
 DR Pfam; PF02058; Guanylin; 1.
 DR PIRSF; PIRSF001849; Guanylin; 1.
 DR PRINTS; PR00774; GUANYLIN.
 DR ProDom; PD005588; Guanylin; 1.
 KW SIGNAL.
 FT SIGNAL 1 27 Potential.
 FT PROPEP 28 89
 FT PEPTIDE 90 113 GCAP-II.
 FT PEPTIDE 98 113 Uroguanylin.
 FT DISULFID 68 81 By similarity.
 FT DISULFID 101 109 By similarity.
 FT DISULFID 104 112 By similarity.
 SQ SEQUENCE 113 AA; 12044 MW; 8160573287BAB642 CRC64;
 Query Match 56.8%; Score 311; DB 1; Length 113;
 Best Local Similarity 59.2%; Pred. No. 7.9e-22;
 Matches 58; Conservative 18; Mismatches 24; Indels 0; Gaps 0;
 QY 9 AVLLLLVLSAQGVYIKYGHFQVLESVKKLEELBEKQMSDPQOKSGLLPDVCYNPALP 68
 Db 15 ALVFLVLLQGTQSVYIQGVFRVQLKSVKLSLDEGQWAPSPRLQAQSPQSVCHSALP 74
 QY 69 LDLPQVCASQAASSTFKALRTIATDECELCINACTGC 106
 Db 75 PDLQPICTSQAASIFQALRTIAGDCELCVNIATGTC 112
 RESULT 8
 GUAY_DIDMA ID GUAY_DIDMA STANDARD; PRT; 109 AA.
 AC Q28358;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Uroguanylin precursor (UGN) (Guanylate cyclase activator 2B).
 GN Name-GUCA2B;
 OS Didelphis marsupialis virginiana (North American opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
 OX NCBI_TaxID=9267;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Fan X., Hamra F.K., Freeman R.H., Eber S.L., Krause W.J., Lim R.W.,
 RA Pace V.M., Currie M.G., Forte L.R.;
 RT "Uroguanylin: cloning of preproguanylin cDNA, mRNA expression in
 RT the intestine and heart and isolation of uroguanylin and
 RT prouroguanylin from plasma."
 RL Biochem. Biophys. Res. Commun. 219:457-462 (1996).
 RN [2]
 RP SEQUENCE OF 95-109.
 RC TISSUE=Urine;
 RA Hamra F.K., Forte L.R., Eber S.L., Pithorodeckyj N.V., Krause W.J.,
 RA Freeman R.H., Chin D.T., Tompkins J.A., Fox K.F., Smith C.E.,
 RA Duffin K.L., Siegel N.R., Currie M.G.;
 RT "Uroguanylin: structure and activity of a second endogenous peptide
 RT that stimulates intestinal guanylate cyclase."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10464-10468 (1993).
 CC -!- FUNCTION: Endogenous activator of intestinal guanylate cyclase. It
 CC stimulates this enzyme through the same receptor binding region as
 CC the heat-stable enterotoxins. May be a potent physiological
 CC regulator of intestinal fluid and electrolyte transport. May be an
 CC autocrine/paracrine regulator of intestinal salt and water

CC transport.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Small and large intestine and atria and
 CC ventricles of heart. Both uroguanylin and prouroguanylin are found
 CC in plasma.
 CC -!- SIMILARITY: Belongs to the guanylin family.
 CC -----
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 CC -----
 CC EMBL; U49353; AAB00553.1; -.
 CC HSSP; Q16661; IUYA.
 CC InterPro; IPR000879; Guanylin.
 CC Pfam; PF02058; Guanylin; 1.
 CC PIRSF; PIRSF001849; Guanylin; 1.
 CC PRINTS; PR00774; GUANYLIN.
 CC ProDom; PD005588; Guanylin; 1.
 CC Direct protein sequencing; Signal.
 KW SIGNAL 1 23 Potential.
 FT PROPEP 24 94 Uroguanylin.
 FT PEPTIDE 95 109 Potential.
 FT DISULFID 65 78 Potential.
 FT DISULFID 98 106 By similarity.
 FT DISULFID 101 109 By similarity.
 SQ SEQUENCE 109 AA; 12040 MW; AE948E210CA3AE7A CRC64;

 CC Query Match 50.8%; Score 278.5; DB 1; Length 109;
 CC Best Local Similarity 55.8%; Pred. No. 1.6e-20;
 CC Matches 55; Conservative 20; Mismatches 23; Indels 1; Gaps 1;

 CC 9 AVLLLLVLSAQGVYIKYHGFQVQLSVKLNLEEKQMSDPQQKSGLLPDV-CYNPAL 67
 CC 11 AMLLVLAQNTQSVYIQYSGFQVQLSVKLNLEELQPSFRHWGTQRDPVSLCSDPAL 70

 CC 68 PDLQPVCSAQEAATFFKALRTIATDELCINVACTGC 106
 CC 71 PSDLPQVCNSQAANIFRALRSISQBDCLCINVACTGC 109

 CC RESULT 9
 CC GUAN_PIG STANDARD; PRT; 109 AA.
 CC ID GUAN_PIG
 CC AC P79897;
 CC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 25-OCT-2004 (Rel. 45, Last annotation update)
 CC DE Guanylin precursor (Guanylate cyclase activator 2A).
 CC GN Name=GUCA2A; Synonym=GUCA2;
 CC OS Sus scrofa (Pig).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC NC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 CC OX NCBI_TaxID=9823;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Jejunum;
 CC RX MEDLINE=99268812; PubMed=10334930; DOI=10.1006/bbrc.1999.0719;
 CC RA Maegert H.J., Hill O., Zucht H.D., Martin S., Meyer M.,
 CC Forssmann W.-G., Adermann K.;
 CC RT "Porcine guanylin and uroguanylin: cDNA sequences, deduced amino acid
 CC sequences, and biological activity of the chemically synthesized
 CC peptides."
 CC RL Biochem. Biophys. Res. Commun. 259:141-148(1999).
 CC -!- FUNCTION: Endogenous activator of intestinal guanylate cyclase. It
 CC stimulates this enzyme through the same receptor binding region as
 CC the heat-stable enterotoxins.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the guanylin family.
 CC -----

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 CC -----
 CC EMBL; Z73607; CAA97974.1; -.
 CC HSSP; Q02747; IGNA.
 CC InterPro; IPR000879; Guanylin.
 CC Pfam; PF02058; Guanylin; 1.
 CC PIRSF; PIRSF001849; Guanylin; 1.
 CC PRINTS; PR00774; GUANYLIN.
 CC ProDom; PD005588; Guanylin; 1.
 KW SIGNAL 1 21 Potential.
 FT PROPEP 22 94
 FT PEPTIDE 95 109 Guanylin.
 FT DISULFID 98 106 By similarity.
 FT DISULFID 101 109 By similarity.
 SQ SEQUENCE 109 AA; 11938 MW; 6368BD1FB0B07A74 CRC64;

 CC Query Match 31.8%; Score 174.5; DB 1; Length 109;
 CC Best Local Similarity 37.5%; Pred. No. 6.3e-10;
 CC Matches 39; Conservative 16; Mismatches 38; Indels 11; Gaps 3;

 CC 6 LMAVALLLVLSAQGVYIKYHGFQVQLSVKLNLEEKQK-SDPQQKSGLLPDVCYN 64
 CC 14 VMAAL-----AGGVTVKDGESFSLSVKLNLEELQPSFRHWGTQRDPVSLCSDPAL 65

 CC 65 PALPDLQPVCSAQEAATFFKALRTIATD--ECLCINVACTGC 106
 CC 66 PKFPBELPICOXNABEILERLETIAODPSTCEICAYAAACGC 109

 CC RESULT 10
 CC Q98TIO PRELIMINARY; PRT; 108 AA.
 CC ID Q98TIO
 CC AC Q98TIO;
 CC DT 01-JUN-2001 (TREMELrel. 17, Created)
 CC DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
 CC DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 CC DE Guanylin.
 CC GN Name=GUCA2I;
 CC OS Anguilla anguilla (European freshwater eel).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 CC OC Anguilla.
 CC OX NCBI_TaxID=7936;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=21139737; PubMed=11243845; DOI=10.1006/bbrc.2001.4485;
 CC RA Comrie M.M., Cutler C.P., Cramb G.;
 CC RT "Cloning and Expression of Guanylin from the European eel (*Anguilla
 CC anguilla*)."
 CC RL Biochem. Biophys. Res. Commun. 281:1078-1085(2001).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RA Comrie M.M.;
 CC RL Thesis (2000), Department of School of Biology, University of St
 CC Andrews, St Andrews, United Kingdom.
 CC DR EMBL; AJ301672; CAC35448.1; -.
 CC DR HSSP; Q02747; IOBR.
 CC DR GO; GO:0008047; F:enzyme activator activity; IEA.
 CC DR InterPro; IPR006058; 2Fe2S fd BS.
 CC DR InterPro; IPR000879; Guanylin.
 CC DR Pfam; PF02058; Guanylin; 1.
 CC PIRSF; PIRSF001849; Guanylin; 1.
 CC PRINTS; PR00774; GUANYLIN.
 CC ProDom; PD005588; Guanylin; 1.
 CC PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN 1.
 CC SEQUENCE 108 AA; 11584 MW; 8A3B6D490E7C858D CRC64;

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OC Anguilla.
OK NCBI_TaxID=7936;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21139737; PubMed=11243845; DOI=10.1006/bbrc.2001.4485;
RA Comrie M.M., Cutler C.P., Cramb G.;
RT "Cloning and Expression of Guanylin from the European eel (Anguilla anguilla).";
RL Biochem. Biophys. Res. Commun. 281:1078-1085(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Comrie M.M.;
RL Thesis (2000), Department of School of Biology, University of St Andrews, St Andrews, United Kingdom.
DR EMBL; AJ301673; CAC35449.1; -.
DR PIR; JC7620; JC7620.
DR HSSP; Q02747; 108R.
GO; GO:0008047; F:enzyme activator activity; IEA.
DR InterPro; IPR006058; 2FeZsfBS.
DR InterPro; IPR000879; Guanylin.
DR Pfam; PF02058; Guanylin; 1.
DR PRSF; PRSFO01849; Guanylin; 1.
DR PRINTS; PR00774; GUANYLIN.
DR ProDom; PD005588; Guanylin; 1.
DR PROSITE; PS00197; 2FEZS-FERREDOXIN; UNKNOWN 1.
SQ SEQUENCE 116 AA; 12547 MW; 38BDAF0AC0B39E0 CRC64;

Query Match      30.6%; Score 167.5; DB 2; Length 116;
Best Local Similarity 41.9%; Pred.No. 3.Se-09;
Matches 44; Conservative 10; Mismatches 44; Indels 7; Gaps 4;

Qy      8 AAVLLLV---LSAQGVYIKYHGFVQLSVVKLANE--LEEKQMSPQQKSGLLPDVCY 63
Db      12 AVLLILAFCLQESQGVWMDGLSPFLAEAVKHLKGANTMSTSHPPNLG-SHAVCS 70
Qy      64 NPALPLDLQVCSAQENASTFKALRTIAT--DECELGINVACTGC 106
Db      71 NPHLPAPFLPCVRREGASALFNRLVDITTPDPCEICANAAGTGC 115

RESULT 13
GUAN_HUMAN
ID _GUAN_HUMAN STANDARD; PRT; 115 AA.
AC Q02747;
DT 01-JUL-1993 (Rel. 26, Created)
DD 01-JUL-1993 (Rel. 26, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DS Guanylin precursor (Guanylate cyclase activator 2A) (Guanylate cyclase activating protein 1) (Gap-I).
GN Name=GUCA2A; Synonyms=GUCA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
FP RP
RC TISSUE=Duoenum;
RX MEDLINE=93011964; PubMed=1327879; DOI=10.1016/0014-5793(92)81387-2;
RA Wiegand R.C., Kato J., Huang M.D., Fok K.F., Kachur J.F., Currie M.G.;
RT "human guanylin: cDNA isolation, structure, and activity.";
RL FEBS Lett. 311:150-154(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=ileum;
RX MEDLINE=93028409; PubMed=1409606;
RA de Sauvage F.J., Keshav S., Kuang W.J., Gillett N., Henzel W., Goeddel D.V.;
RA RA
RT "Precursor structure, expression, and tissue distribution of human guanylin.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:9089-9093(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX RC

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RX MEDLINE=95199289; PubMed=7892222;
 RA Hill O., Kuhn M., Zucht H.D., Cetin Y., Kulaksiz H., Adermann K.,
 RA Klock G., Reckemmer G., Forssmann W.-G., Magert H.J.,
 RT "Analysis of the human guanylin gene and the processing and cellular
 RT localization of the peptide."
 RL Proc. Natl. Acad. Sci. U.S.A. 92:2046-2050(1995).
 RN [4]
 RN SEQUENCE OF 22-68.
 RP MEDLINE=93178628; PubMed=8095028; DOI=10.1016/0014-5793(93)80022-M;
 RX Kuhn M., Rada M., Adermann K., Schulz-Knappe P., Gerzer R.,
 RA Heim J.-M., Forssmann W.-G.;
 RT "The circulating bioactive form of human guanylin is a high molecular
 RT weight peptide (10.3 kDa)."
 RN FEBS Lett. 318:205-209(1993).
 RN [5]
 RP STRUCTURE BY NMR OF 101-115.
 RX MEDLINE=95034794; PubMed=7947768;
 RA Skelton N.J., Garcia K.C., Goeddel D.V., Quan C., Burnier J.P.;
 RT "determination of the solution structure of the peptide hormone
 RT guanylin: observation of a novel form of topological
 RT stereoisomerism."
 RL Biochemistry 33:13581-13592(1994).
 CC -!- FUNCTION: Endogenous activator of intestinal guanylate cyclase. It
 CC stimulates this enzyme through the same receptor binding region as
 CC the heat-stable enterotoxins.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Highly expressed in ileum and colon. Found in
 CC plasma.
 CC -!- SIMILARITY: Belongs to the guanylin family.
 CC -----
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 CC -----
 DR EMBL; M97496; AAA35915.1; -;
 DR EMBL; M95174; AAA58625.1; -;
 DR EMBL; X74322; CAC22258.1; -;
 DR PIR; A46279; A46279.
 DR PDB; 1GNA; NMR; @=103-115.
 DR PDB; 1GNB; NMR; @=103-115.
 DR PDB; 1ORR; NMR; A=22-115.
 DR Genew; HGNC:4682; GUC2A.
 DR MIM; 133392; -;
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0030250; F:guanylate cyclase activator activity; NAS.
 DR GO; GO:0003179; F:hormone activity; NAS.
 DR GO; GO:0007165; P:signal transduction; NAS.
 DR InterPro; IPR000879; Guanylin.
 DR Pfam; PF02058; Guanylin; 1.
 DR PIRSF; PIRSF001849; Guanylin; 1.
 DR PRINTS; PR00774; GUANYLIN.
 DR ProDom; PD005588; Guanylin; 1.
 DR 3D-structure; Direct protein sequencing; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 115 HMW-guanylin.
 FT PEPTIDE 101 115 Guanylin.
 FT DISULFID 104 112
 FT DISULFID 107 115
 FT TURN 104 107
 FT TURN 110 111
 SQ SEQUENCE 115 AA; 12448 MW; C644C03BAFFC26FA CRC64;
 Query Match 30.4%; Score 166.5; DB 1; Length 115;
 Best Local Similarity 35.1%; Pred. No. 4.4e-09;
 Matches 40; Conservative 15; Mismatches 32; Indels 27; Gaps 4;
 QY 7 WAAVLLLVLSQAGVYIKYHGFQVLESVKKLNLEBKQMSDPQOQKSG-----56
 DB 15 WAAV-----AGGVTVQGNFSGFLESVKKLNLEBKQMSDPQOQKSG-----56

QY 57 --LLPDVVCNFPALPDLQPVCAQEAASFTFKALRTIATD--ECELINVACTGC 106
 DB 62 BPVVILCSNPNFPPELKLPLCKEPNAQELQRLERAEADPGTCEICAYAACTGC 115
 RESULT 14
 Q7ZS1
 ID Q7ZS1 PRELIMINARY; PRT; 110 AA.
 AC Q7ZS1;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Preprorenoguanilin.
 GN Name=renoguanilin.
 OS Anguilla japonica (Japanese eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 OC Anguilla.
 OX NCBI_TaxID=7937;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=22692502; PubMed=12684514; DOI=10.1074/jbc.M303111200;
 RA Yuge S., Inoue K., Hyodo S., Takei Y.;
 RT "A novel guanylin family (guanylin, uroguanylin, and renoguanilin) in
 RT eels: possible osmoregulatory hormones in intestine and kidney."
 RL J. Biol. Chem. 278:22726-22733(2003).
 DR EMBL; AB080641; BAC76010.1; -;
 DR HSP; Q02747; 108R.
 DR GO; GO:0008047; F:enzyme activator activity; IEA.
 DR InterPro; IPR006058; 2Fe2S fd BS.
 DR InterPro; IPR000879; Guanylin.
 DR Pfam; PF02058; Guanylin; 1.
 DR PIRSF; PIRSF001849; Guanylin; 1.
 DR PRINTS; PR00774; GUANYLIN.
 DR ProDom; PD005588; Guanylin; 1.
 DR PROSITE; PS00197; 2FE2S FERREDOXIN; UNKNOWN 1.
 SQ SEQUENCE 110 AA; 11676 MW; B161A03A913894F9 CRC64;
 Query Match 27.5%; Score 150.5; DB 2; Length 110;
 Best Local Similarity 39.2%; Pred. No. 1.8e-07;
 Matches 40; Conservative 15; Mismatches 38; Indels 9; Gaps 4;
 QY 10 VLLLVLSQAGVYIKYHGFQVLESVKKLNLEBKQMS---DPOQKSGLLPDVCNPA 66
 DB 12 VALALVTEAVQ---VEEGSFPLDAVKKLELMGVDMTVKQSPRLAKTSTTA-VCTNPD 67
 QY 67 LPDLQPVCAQEAASFTFKALRTIA--TDECELINVACTGC 106
 DB 68 LPVFLPLCKSKGAANSFFRLGFAARADLCICAFAACTGC 109
 RESULT 15
 GUAN_CAVPO
 ID GUAN_CAVPO STANDARD; PRT; 107 AA.
 AC P70664;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Guanylin precursor (Guanylate cyclase activator 2A).
 GN Name=GUC2A2; Synonyms=GUCA2;
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Kruhoffer M., Cetin Y., Kaempf U., Forssmann W.-G.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Endogenous activator of intestinal guanylate cyclase. It
 CC stimulates this enzyme through the same receptor binding region as


```

CC the heat-stable enterotoxins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the guanylin family.
CC -----
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CC -----
DR EMBL; Z74736; CAA98991.1; -.
DR EMBL; Z74737; CAA98992.1; -.
DR HSSP; Q02747; IGNA.
DR InterPro; IPR000879; Guanylin.
DR Pfam; PF02058; Guanylin; 1.
DR PIRSF; PIRSF001849; Guanylin; 1.
DR PRINTS; PR00774; GUANYLIN.
DR ProDom; PD005588; Guanylin; 1.
KW Signal.
FT SIGNAL 1 20 Potential.
FT PROPEP 21 92
FT PEPTIDE 93 107 Guanylin.
FT DISULFID 96 104 By similarity.
FT DISULFID 99 107 By similarity.
SQ SEQUENCE 107 AA; 11483 MW; C4BE4CE609409F45 CRC64;

Query Match 27.2%; Score 149; DB 1; Length 107;
Best Local Similarity 33.3%; Pred. No. 2.5e-07;
Matches 34; Conservative 14; Mismatches 44; Indels 10; Gaps 2;

Qy 7 WAAVLLLLVLQSAQGVYIKYHGFQVQLSEVKKLNELEEKQMSDPQQQKSGLLPDVCYNPA 66
Db 14 WAALVGAVTVQDGD-----FSPSLESVKKLDQEAPEKVKQGRKFKVAPPLCSFSG 65

Qy 67 LPDLQPVCSAQEAATPKALRTIATD--ECELINVACTGC 106
Db 66 FPEELRPVKPEPNQDILNRLAVIAQDPSTCEICAYACAGC 107

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Search completed: March 26, 2005, 16:48:35
Job time : 92.2993 secs

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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:35:58 ; Search time 122.628 Seconds
(without alignments)
353.241 Million cell updates/sec

Title: US-10-775-481A-56
Perfect score: 579
Sequence: 1 MGCRAAGSLPGVAVVLL.....RTIANDCELCVNVACTGCL 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	100.0	112	2	AAW18498 Human GCA
2	579	100.0	112	2	AAW10595 Guanylate
3	579	100.0	112	6	ABG74823 Human uro
4	579	100.0	112	8	ADR45875 Amino aci
5	554	95.7	108	2	AAW18467 Human GCA
6	554	95.7	108	2	AAW18478 Human GCA
7	554	95.7	108	2	AAW23221 GCAP-II C
8	445	76.9	84	2	AAW18484 Human GCA
9	445	76.9	84	2	AAW23232 GCAP-II C
10	429	74.1	81	2	AAW18485 Human GCA
11	429	74.1	81	2	AAW23233 GCAP-II C
12	412	71.2	78	2	AAW18486 Human GCA
13	412	71.2	78	2	AAW23234 GCAP-II C
14	407	70.3	77	2	AAW18468 Human GCA
15	407	70.3	77	2	AAW18479 Human GCA
16	407	70.3	77	2	AAW23222 GCAP-II C
17	389	67.2	73	2	AAW18490 Human GCA
18	389	67.2	73	2	AAW23237 GCAP-II C
19	375	64.8	70	2	AAW18471 Human GCA
20	375	64.8	70	2	AAW18480 Human GCA
21	375	64.8	70	2	AAW23225 GCAP-II C
22	370	63.9	69	2	AAW18472 Human GCA
23	370	63.9	69	2	AAW18481 Human GCA
24	370	63.9	69	2	AAW23226 GCAP-II C
25	362	62.5	67	2	AAW18474 Human GCA

ALIGNMENTS

RESULT 1

AAW18498	26	362	62.5	67	2	AAW23228	GCAP-II C
XX	27	360	62.2	69	2	AAW18488	Human GCA
AC	28	356	61.5	66	2	AAW18491	Human GCA
XX	29	356	61.5	66	2	AAW23238	GCAP-II C
DT	30	356	61.5	106	8	ADR45874	Amino aci
XX	31	347	59.9	64	2	AAW18492	Human GCA
DE	32	347	59.9	64	2	AAW23239	GCAP-II C
XX	33	300	51.8	56	2	AAW18469	Human GCA
XX	34	300	51.8	56	2	AAW23223	GCAP-II C
KW	35	252	43.5	109	6	ABG74824	Oposaum 1
XX	36	230	39.7	43	2	AAW18489	Human GCA
OS	37	230	39.7	43	2	AAW23236	GCAP-II C
PN	38	216	37.3	85	3	AAW53987	Human col
XX	39	203	35.1	38	2	AAW18475	Human GCA
PD	40	203	35.1	38	2	AAW23229	GCAP-II C
XX	41	197	34.0	37	2	AAW18493	Human GCA
XX	42	197	34.0	37	2	AAW23240	GCAP-II C
XX	43	164.5	28.4	115	7	ADJ18912	Human NOV
XX	44	162.5	28.1	94	2	AAW62442	Guanylate
XX	45	162.5	28.1	94	2	AAW69810	Expressio

This sequence represents a precursor of the guanyl cyclase C activating peptide, GCAP-II, which affects insulin secretion by the beta cells in the pancreas. This peptide is useful for treating pancreatic endocrine disorders, especially diabetes mellitus type II, renal and intestinal disorders, disorders of the gastrointestinal, respiratory and urogenital apparatus, disorders of the cardiovascular and nervous systems, disorders of the integuments and sense organs and diseases associated with GCAP-II (89-112) deficiency. This peptide can be used for treatment of electrolyte effects on bone reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP-II (89-112) can be used to treat diseases associated with overproduction of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP-I (99-15) cDNA are useful for diagnosis and treatment of the above disorders e.g. gene therapy for diabetes

XX SQ Sequence 112 AA;
Query Match 100.0%; Score 579; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.5e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGCRAASGLPGVAVVLLLLQSTQSVYIQGFRVQLSMKLSDLAQWAPSRLQAO 60
DB 1 MGCRAASGLPGVAVVLLLLQSTQSVYIQGFRVQLSMKLSDLAQWAPSRLQAO 60
QY 61 SLLPAVCHHPALPDQLQPCVQASQASISFKTLRTIANDDCCLCVNACTGCL 112
DB 61 SLLPAVCHHPALPDQLQPCVQASQASISFKTLRTIANDDCCLCVNACTGCL 112
RESULT 2
AAW10595
ID AAW10595 standard; protein; 112 AA.
XX AAW10595;
AC AAW10595;
XX 29-OCT-1997 (first entry)
XX Guanylate cyclase activating peptide II.
XX Human; guanylate cyclase; activating peptide; GCAP-II; cGMP;
XX trans epithelial transport; treatment; kidney; intestinal; respiratory;
XX urogenital; circulatory; nervous system; disorder; disease; endocrine;
XX sensory; system; osteoporosis; dental; pancreas; diabetes; hypophysis;
XX gastrointestinal tract; diarrhoea; gene therapy; probe;
XX recombinant production; transgenic animal; antibody; immunoassay reagent.
XX OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..88
FT /label= sig_peptide
FT 89..112
FT /label= mat_peptide
XX DE19528544-Al.
XX 06-FEB-1997.
XX 03-AUG-1995; 95DE-01028544.
XX 03-AUG-1995; 95DE-01028544.
XX (FORS/) FORSMANN W.
XX Forsmann W;
XX WPI; 1997-110032/11.
XX N-PSDB; AAT60819.
XX Guanylate cyclase activating peptide II - increases cGMP formation, and
XX controls transport of water and electrolytes across epithelial cells.
XX Claim 1; Page 4; 15pp; German.
XX The present sequence is the human guanylate cyclase activating peptide II
XX (GCAP-II), which increases cGMP formation, and is involved in the control
XX of trans epithelial water and electrolyte transport. GCAP-II can be used
XX to treat a variety of kidney, intestinal, respiratory, urogenital, and
XX circulatory and nervous system disorders, diseases of the endocrine and
XX sensory systems (e.g. osteoporosis, and dental disease), disorders of the
XX pancreas (e.g. diabetes, and hypophysis) or the endocrine
XX gastrointestinal tract and for the long term treatment of diarrhoea,
XX without inducing an immune response. The GCAP-II cDNA can be used to
XX treat the same conditions, clone the GCAP-II-encoding gene for use in
XX gene therapy, as a hybridisation probe and for the production of
XX recombinant GCAP-II or transgenic animal creation. Antibodies raised

CC against GCAP-II are useful as immunoassay reagents. GCAP-II is
CC administered at, e.g. 100-1200 microg/day by intravenous or intramuscular
CC injection or 300-1200 microg/day subcutaneously. It may also be given
CC orally, intranasally or by inhalation, in typical unit doses of 0.3-30
CC mg. GCAP-II was chemically synthesised, or isolated by chromatography
CC from transformed eukaryotic or prokaryotic cells, or human blood. When
CC T84 cells were incubated with synthetic GCAP-II, generation of cGMP was
CC increased in a dose dependent manner. GCAP-II influences cGMP production
CC via a known receptor for heat stable enterotoxin. Other stomach,
CC intestinal, pancreatic and liver cells also responded to GCAP-II, e.g.
CC via changes in intracellular Ca²⁺ ion concentration
XX SQ Sequence 112 AA;
Query Match 100.0%; Score 579; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.5e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGCRAASGLPGVAVVLLLLQSTQSVYIQGFRVQLSMKLSDLAQWAPSRLQAO 60
DB 1 MGCRAASGLPGVAVVLLLLQSTQSVYIQGFRVQLSMKLSDLAQWAPSRLQAO 60
QY 61 SLLPAVCHHPALPDQLQPCVQASQASISFKTLRTIANDDCCLCVNACTGCL 112
DB 61 SLLPAVCHHPALPDQLQPCVQASQASISFKTLRTIANDDCCLCVNACTGCL 112

RESULT 3
ABG74823
ID ABG74823 standard; protein; 112 AA.
XX ABG74823;
AC ABG74823;
XX 12-JUN-2003 (first entry)
XX Human uroguanylin precursor SEQ ID 5.
XX Apical membrane; mucosal epithelial cell; respiratory tract;
XX guanylate cyclase C; G protein-coupled receptor; guanosine triphosphate;
XX cyclic guanosine monophosphate; cGMP; chloride ion secretion; inhalation;
XX membrane-associated type II protein kinase; mucus fluidisation;
XX cystic fibrosis transmembrane conductance regulator; breathing disorder;
XX mucus secretion; antiasthmatic; antiinflammatory; bronchial asthma;
XX chronic bronchitis; cystic fibrosis; uroguanylin; human.
XX OS Homo sapiens.
XX WO200298912-A2.
XX 12-DEC-2002.
XX 05-JUN-2002; 2002WO-DE002040.
XX 05-JUN-2001; 2001DE-01027119.
XX (CETI/) CETIN Y.
XX (SAVA/) SAVAS Y.
XX Cetin Y, Savas Y;
XX WPI; 2003-156842/15.
XX Composition useful for treating respiratory disease, comprises a peptide
XX that activates guanylate cyclase C, and is delivered to the apical
XX membrane through the respiratory tract.
XX Claim 3; Page 3; 23pp; German.

XX This invention describes a novel medicament in a formulation that is
XX delivered to the apical membrane of mucosal epithelial cells through the
XX respiratory tract. The medicament contains at least one peptide that
XX activates guanylate cyclase C (GCC). GCC is a G protein-coupled receptor
XX that catalyses conversion of guanosine triphosphate to cyclic guanosine

CC monophosphate (cGMP) and is present on the apical (air) side of
 CC respiratory epithelial cells but not on the basolateral (blood) side.
 CC cGMP activates membrane-associated type II protein kinase which in turn
 CC activates the regulatory domain of the cystic fibrosis transmembrane
 CC conductance regulator, resulting in secretion of chloride ions and water
 CC from the cells, causing fluidisation of the mucus. The products of the
 CC invention are used to make an inhalation device containing the medicament
 CC for diagnosing diseases that are accompanied by breathing disorders or
 CC disorders of mucus secretion in the respiratory tract, by detecting at
 CC least one GCC activator. The products of the invention have antiasthmatic
 CC and antiinflammatory activity. The method is useful for diagnosing and
 CC treating diseases accompanied by breathing disorders or disorders of
 CC mucus secretion in the respiratory tract particularly bronchial asthma,
 CC chronic bronchitis and cystic fibrosis. The product of the invention
 CC improves fluidity and evacuation of bronchial mucus and acts locally
 CC (since the medicament does not enter the bloodstream), so systemic side
 CC effects are minimised. Only very small doses of the medicament are
 CC required. This sequence represents a precursor of the human guanylate
 CC cyclase C activator peptide, uroguanylin, described in the disclosure of
 CC the invention

XX SQ Sequence 112 AA;

Query Match 100.0%; Score 579; DB 6; Length 112;

Best Local Similarity 100.0%; Pred. No. 4.5e-57;

Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGCRAASGLPGVAVVLLLLQLQSTQSVYIQGFRVQLESMMKLSDLQAQWAPSRLQAO 60

Db 1 MGCRAASGLPGVAVVLLLLQLQSTQSVYIQGFRVQLESMMKLSDLQAQWAPSRLQAO 60

Qy 61 SLLPAVCHHPALPDQLPVCASQEAASSIFKTLRTIANDDCLCVNVACTGCL 112

Db 61 SLLPAVCHHPALPDQLPVCASQEAASSIFKTLRTIANDDCLCVNVACTGCL 112

RESULT 4

ADR45875

ID ADR45875 standard; peptide; 112 AA.

AC ADR45875;

DT 18-NOV-2004 (first entry)

XX Amino acid sequence of ST receptor ligand uroguanylin.

XX heat stable toxin; ST; ST receptor; colorectal cancer; gastric cancer;

XX oesophageal cancer; colorectal cell; gastric cell; oesophageal cell;

XX uroguanylin.

XX Homo sapiens.

XX WO2004071436-A2.

XX 26-AUG-2004.

XX 10-FEB-2004; 2004WO-US003765.

XX 10-FEB-2003; 2003US-0446730P.

XX (UYUE-) UNIV JEFFERSON THOMAS.

XX Waldman SA, Pitari GM, Park J, Schulz S, Wolfe HR;

XX WPI; 2004-615913/59.

XX Increasing ST receptor molecules on the surface of a colorectal, gastric
 PT or oesophageal cancer cell to treat these cancers comprises administering
 PT ST receptor ligand molecules that bind to ST receptors on the surface of
 PT the cancer cell.

XX Claim 6; SEQ ID NO 56; 97pp; English.

XX

CC The specification describes a method for increasing the number of heat
 CC stable toxin (ST) receptor molecules on the surface of a metastasised
 CC colorectal cancer cell. The method comprises administering, by continuous
 CC infusion, at least 0.1 nM of an ST receptor ligand per 10 kg bodyweight
 CC per hour for at least 6 hours, where ST receptor ligand molecules bind to
 CC ST receptors on the surface of the cancer cell in the individual and the
 CC number of ST receptor molecules on the surface of the cancer cell is
 CC increased. Therapeutic compositions comprising components which target ST
 CC receptors can then be used to inhibit proliferation of the colorectal,
 CC gastric and oesophageal cells. This method may be used for treating
 CC individuals that have diseases that affect colorectal, gastric and
 CC oesophageal cells, including colorectal, gastric or oesophageal cancers.
 CC The present sequence represents a ST receptor ligand used in the method
 CC of the invention, designated uroguanylin.

XX SQ Sequence 112 AA;

Query Match 100.0%; Score 579; DB 8; Length 112;

Best Local Similarity 100.0%; Pred. No. 4.5e-57;

Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGCRAASGLPGVAVVLLLLQLQSTQSVYIQGFRVQLESMMKLSDLQAQWAPSRLQAO 60

Db 1 MGCRAASGLPGVAVVLLLLQLQSTQSVYIQGFRVQLESMMKLSDLQAQWAPSRLQAO 60

Qy 61 SLLPAVCHHPALPDQLPVCASQEAASSIFKTLRTIANDDCLCVNVACTGCL 112

Db 61 SLLPAVCHHPALPDQLPVCASQEAASSIFKTLRTIANDDCLCVNVACTGCL 112

RESULT 5

AAW18467

ID AAW18467 standard; peptide; 108 AA.

AC AAW18467;

XX 23-APR-1998 (first entry)

XX Human GCAP-II (89-112) endoprotease Arg-C digested fragment 1.

XX Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic;

XX diabetes; endocrine disorder; diagnosis; treatment; human.

XX Homo sapiens.

XX DE19543628-A1.

XX 28-MAY-1997.

XX 24-NOV-1995; 95DE-01043628.

XX 24-NOV-1995; 95DE-01043628.

XX (FORS/) FORSMANN W.

XX Forssmann W, Kist A, Kruhoffer M, Meyer M, Pardigol A, Heine G;

XX WPI; 1997-290350/27.

XX New guanyl cyclase C activating peptide fragments - have insulinotropic
 PT activity, useful for treating diabetes, etc.

XX Claim 3; Fig 3; 33pp; German.

XX Peptides AAW18467-W18470 represent fragments of the guanyl cyclase C

CC activating peptide, GCAP-II, obtained by digestion with endoprotease Arg-

CC C. GCAP-II is involved in insulin secretion by pancreatic beta cells.

CC This peptide fragment could be used to which affects insulin secretion by

CC the beta cells treat pancreatic endocrine disorders, especially diabetes

CC mellitus type II, renal and intestinal disorders, disorders of the

CC gastrointestinal, respiratory and urogenital apparatus, disorders of the

CC cardiovascular and nervous systems, disorders of the integuments and

CC sense organs and diseases associated with GCAP II (89-112) deficiency.

CC This peptide can be used for treatment of electrolyte effects on bone
 CC reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP
 CC -II (89-112) can be used to treat diseases associated with overproduction
 CC of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP I (99-15) cDNA are
 CC useful for diagnosis and treatment of the above disorders e.g. gene
 CC therapy for diabetes
 XX
 SQ Sequence 108 AA;

Query Match 95.7%; Score 554; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 2.8e-54;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 AASGLLPQVAVVLLLLQSTQSVYIQGFRVQLESMMKLSLEAQWAPSPRLQASLLP 64
 DB 1 AASGLLPQVAVVLLLLQSTQSVYIQGFRVQLESMMKLSLEAQWAPSPRLQASLLP 60
 QY 65 AVCHHPALPQDLPQVCASQESASSIFKTLRTIANDDCELCVNVACTGCL 112
 DB 61 AVCHHPALPQDLPQVCASQESASSIFKTLRTIANDDCELCVNVACTGCL 108

RESULT 6
 AAW18478
 ID AAW18478 standard; peptide; 108 AA.
 AC AAW18478;
 XX
 XX
 DT 22-APR-1998 (first entry)
 XX
 DE Human GCAP-II (89-112) trypsin digested fragment 1.
 XX
 KW Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic;
 KW diabetes; endocrine disorder; diagnosis; treatment; human.
 XX
 OS Homo sapiens.
 XX
 PN DE19543628-A1.
 XX
 XX 28-MAY-1997.
 XX
 XX 24-NOV-1995; 95DE-01043628.
 XX
 XX 24-NOV-1995; 95DE-01043628.
 XX
 XX (FORS/) FORSSMANN W.
 XX
 XX Forssmann W, Kist A, Kruhoeffler M, Meyer M, Pardigol A, Heine G;
 XX WPI; 1997-290350/27.
 XX
 XX New guanyl cyclase C activating peptide fragments - have insulinotropic
 XX activity, useful for treating diabetes, etc.
 XX
 XX Claim 3; Fig 3; 33pp; German.

XX Peptides AAW18478-W18483 represent fragments of the guanyl cyclase C
 XX activating peptide, GCAP-II, obtained by digestion with trypsin. GCAP-II
 XX is involved in insulin secretion by pancreatic beta cells. This peptide
 XX fragment could be used to which affects insulin secretion by the beta
 XX cells treat pancreatic endocrine disorders, especially diabetes mellitus
 XX type II, renal and intestinal disorders, disorders of the respiratory,
 XX gastrointestinal and urogenital apparatus, disorders of the
 XX cardiovascular and nervous systems, disorders of the integuments and
 XX sense organs and diseases associated with GCAP II (89-112) deficiency.
 XX This peptide can be used for treatment of electrolyte effects on bone
 XX reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP
 XX -II (89-112) can be used to treat diseases associated with overproduction
 XX of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP I (99-15) cDNA are
 XX useful for diagnosis and treatment of the above disorders e.g. gene
 XX therapy for diabetes
 XX
 SQ Sequence 108 AA;

Query Match 95.7%; Score 554; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 2.8e-54;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 AASGLLPQVAVVLLLLQSTQSVYIQGFRVQLESMMKLSLEAQWAPSPRLQASLLP 64
 DB 1 AASGLLPQVAVVLLLLQSTQSVYIQGFRVQLESMMKLSLEAQWAPSPRLQASLLP 60
 QY 65 AVCHHPALPQDLPQVCASQESASSIFKTLRTIANDDCELCVNVACTGCL 112
 DB 61 AVCHHPALPQDLPQVCASQESASSIFKTLRTIANDDCELCVNVACTGCL 108

RESULT 7
 AAW23221
 ID AAW23221 standard; peptide; 108 AA.
 AC AAW23221;
 XX
 XX
 DT 29-OCT-1997 (first entry)
 XX
 DE GCAP-II C-terminal fragment prepared by endoproteinase Arg-C.
 XX
 KW Human; guanylate cyclase; activating peptide; GCAP-II; cGMP;
 KW trans epithelial transport; treatment; kidney; intestinal; respiratory;
 KW urogenital; circulatory; nervous system; disorder; disease; endocrine;
 KW sensory; system; osteoporosis; dental; pancreas; diabetes; hypophysis;
 KW gastrointestinal tract; diarrhoea; gene therapy; probe;
 KW recombinant production; transgenic animal; antibody; immunoassay reagent.
 XX
 OS Homo sapiens.
 XX
 PN DE19528544-A1.
 XX
 PD 06-FEB-1997.
 XX
 PF 03-AUG-1995; 95DE-01028544.
 XX
 PR 03-AUG-1995; 95DE-01028544.
 XX
 XX (FORS/) FORSSMANN W.
 XX
 XX Forssmann W;
 XX WPI; 1997-110032/11.
 XX
 XX Guanylate cyclase activating peptide II - increases cGMP formation, and
 XX controls transport of water and electrolytes across epithelial cells.
 XX
 XX Claim 3; Page 4-5; 15pp; German.

XX The present sequence is a carboxy-terminal fragment of the human
 XX guanylate cyclase activating peptide II (GCAP-II) precursor, prepared by
 XX endoproteolytic cleavage with endoproteinase Arg-C. GCAP-II increases
 XX cGMP formation, and is involved in the control of trans epithelial water
 XX and electrolyte transport. GCAP-II can be used to treat a variety of
 XX kidney, intestinal, respiratory, urogenital, circulatory and nervous
 XX system disorders, diseases of the endocrine and sensory systems (e.g.
 XX osteoporosis, and dental disease), disorders of the pancreas (e.g.
 XX diabetes, and hypophysis) or the endocrine gastrointestinal tract and for
 XX the long term treatment of diarrhoea, without inducing an immune
 XX response. The GCAP-II cDNA can be used to treat the same conditions,
 XX clone the GCAP-II-encoding gene for use in gene therapy, as a
 XX hybridisation probe and for the production of recombinant GCAP-II or
 XX transgenic animal creation. Antibodies raised against GCAP-II are useful
 XX as immunoassay reagents. GCAP-II, or a fragment, are administered at,
 XX e.g. 100-1200 microg/day by intravenous or intramuscular injection or 300
 XX -1200 microg/day subcutaneously. They may also be given orally,
 XX intranasally or by inhalation, in typical unit doses of 0.3-30 mg. GCAP-
 XX II was chemically synthesised, or isolated by chromatography from
 XX transformed eukaryotic or prokaryotic cells, or human blood. When T84
 XX cells were incubated with synthetic GCAP-II, generation of cGMP was

increased in a dose dependent manner. GCAP-II influences cGMP production via a known receptor for heat stable enterotoxin. Other stomach, intestinal, pancreatic and liver cells also responded to GCAP-II, e.g. via changes in intracellular Ca²⁺ ion concentration

Sequence 108 AA;

Query Match 95.7%; Score 554; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8e-54;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AASGLPGVAVVLLLLQSTQSVVYIQGFRVQLESMMKLSDLAQWAPSRLQAOQLLP 64
Dy 1 AASGLPGVAVVLLLLQSTQSVVYIQGFRVQLESMMKLSDLAQWAPSRLQAOQLLP 60
Qy 65 AVCHHPALPQDLQPVCAQSEASSIFKTLRTIANDDCELCVNVACTGCL 112
Dy 61 AVCHHPALPQDLQPVCAQSEASSIFKTLRTIANDDCELCVNVACTGCL 108

RESULT 8
AAW18484
ID AAW18484 standard; peptide; 84 AA.

AC AAW18484;

XX 22-APR-1998 (first entry)

DE Human GCAP-II (89-112) chymotrypsin digested fragment 1.

XX Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic;
KW diabetes; endocrine disorder; diagnosis; treatment; human.

OS Homo sapiens.

XX DE19543628-AL.

XX 28-MAY-1997.

XX 24-NOV-1995; 95DE-01043628.

XX 24-NOV-1995; 95DE-01043628.

XX (FORS/) FORSMANN W.

XX Forsemann W, Kist A, Kruhoeffer M, Meyer M, Pardigol A, Heine G;

XX WPI; 1997-290350/27.

XX New guanyl cyclase C activating peptide fragments - have insulinotropic activity, useful for treating diabetes, etc.

XX Claim 3; Fig 3; 33pp; German.

XX Peptides AAW18484-W18487 represent fragments of the guanyl cyclase C activating peptide, GCAP-II, obtained by digestion with chymotrypsin. GCAP-II is involved in insulin secretion by pancreatic beta cells. This peptide fragment could be used to which affects insulin secretion by the beta cells treat pancreatic endocrine disorders, especially diabetes mellitus type II, renal and intestinal disorders, disorders of the respiratory, gastrointestinal and urogenital apparatus, disorders of the cardiovascular and nervous systems, disorders of the integuments and sense organs and diseases associated with GCAP II (89-112) deficiency. This peptide can be used for treatment of electrolyte effects on bone reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP -II (89-112) can be used to treat diseases associated with overproduction of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP I (99-15) cDNA are useful for diagnosis and treatment of the above disorders e.g. gene therapy for diabetes

XX Sequence 84 AA;

Query Match 76.9%; Score 445; DB 2; Length 84;

Best Local Similarity 100.0%; Pred. No. 3.9e-42;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 IOYQGFVQLESMMKLSDLAQWAPSRLQAOQLLPVCHHPALPQDLQPVCAQSEASSI 88
Dy 1 IOYQGFVQLESMMKLSDLAQWAPSRLQAOQLLPVCHHPALPQDLQPVCAQSEASSI 60

Qy 89 FXTLRTIANDDCELCVNVACTGCL 112

Dy 61 FXTLRTIANDDCELCVNVACTGCL 84

RESULT 9
AAW23232
ID AAW23232 standard; peptide; 84 AA.

XX AAW23232;

XX 29-OCT-1997 (first entry)

DE GCAP-II C-terminal fragment prepared by chymotrypsin.

XX Human; guanylate cyclase; activating peptide; GCAP-II; cGMP;
KW transepithelial transport; treatment; kidney; intestinal; respiratory;
KW urogenital; circulatory; nervous system; disorder; disease; endocrine;
KW sensory; system; osteoporosis; dental; pancreas; diabetes; hypophysis;
KW gastrointestinal tract; diarrhoea; gene therapy; probe;
KW recombinant production; transgenic animal; antibody; immunoassay reagent.

OS Homo sapiens.

XX DE19528544-AL.

XX 06-FEB-1997.

XX 03-AUG-1995; 95DE-01028544.

XX 03-AUG-1995; 95DE-01028544.

XX (FORS/) FORSMANN W.

XX Forsemann W;

XX WPI; 1997-110032/11.

XX Guanylate cyclase activating peptide II - increases cGMP formation, and controls transport of water and electrolytes across epithelial cells.

XX Claim 3; Page 6; 15pp; German.

XX The present sequence is a carboxy-terminal fragment of the human guanylate cyclase activating peptide II (GCAP-II) precursor, prepared by endoproteolytic cleavage with chymotrypsin. GCAP-II increases cGMP formation, and is involved in the control of transepithelial water and electrolyte transport. GCAP-II can be used to treat a variety of kidney, intestinal, respiratory, urogenital, circulatory and nervous system disorders, diseases of the endocrine and sensory systems (e.g. osteoporosis, and dental disease), disorders of the pancreas (e.g. diabetes, and hypophysis) or the endocrine gastrointestinal tract and for the long term treatment of diarrhoea, without inducing an immune response. The GCAP-II cDNA can be used to treat the same conditions, clone the GCAP-II-encoding gene for use in gene therapy, as a hybridization probe and for the production of recombinant GCAP-II or transgenic animal creation. Antibodies raised against GCAP-II or as immunoassay reagents. GCAP-II, or a fragment, are administered at, e.g. 100-1200 microg/day by intravenous or intramuscular injection or 300 -1200 microg/day subcutaneously. They may also be given orally, intranasally or by inhalation, in typical unit doses of 0.3-30 mg. GCAP-II was chemically synthesised, or isolated by chromatography from transformed eukaryotic or prokaryotic cells, or human blood. When T84 cells were incubated with synthetic GCAP-II, generation of cGMP was increased in a dose dependent manner. GCAP-II influences cGMP production via a known receptor for heat stable enterotoxin. Other stomach,

CC intestinal, pancreatic and liver cells also responded to GCAP-II, e.g.
 CC via changes in intracellular Ca2+ ion concentration
 SQ Sequence 84 AA;
 Query Match 76.9%; Score 445; DB 2; Length 84;
 Best Local Similarity 100.0%; Pred. No. 3.9e-42;
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 IQQFRVQLSEMKKLSLEAQWAPSPRLQAQSLPVAVCHHPALPDQLQPVCAQSEASSI 88
 DB 1 IQQFRVQLSEMKKLSLEAQWAPSPRLQAQSLPVAVCHHPALPDQLQPVCAQSEASSI 60
 QY 89 FKTIRTIANDDCELCVNVACTGCL 112
 DB 61 FKTIRTIANDDCELCVNVACTGCL 84

RESULT 10
 AAW18485
 ID AAW18485 standard; peptide; 81 AA.
 AC AAW18485;
 DT 22-APR-1998 (first entry)
 XX Human GCAP-II (89-112) chymotrypsin digested fragment 2.
 KW Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic;
 KW diabetes; endocrine disorder; diagnosis; treatment; human.
 XX Homo sapiens.
 OS Homo sapiens.
 PN DE19543628-A1.
 PD 28-MAY-1997.
 XX 24-NOV-1995; 95DE-01043628.
 XX 24-NOV-1995; 95DE-01043628.
 PA (FORS/) FORSSMANN W.
 PI Forssmann W, Kist A, Kruhoffer M, Meyer M, Pardigol A, Heine G;
 XX WPI; 1997-290350/27.
 XX New guanyl cyclase C activating peptide fragments - have insulinotropic
 PT activity, useful for treating diabetes, etc.
 PS Claim 3; Fig 3; 33pp; German.
 XX Peptides AAW18484-W18487 represent fragments of the guanyl cyclase C
 CC activating peptide, GCAP-II, obtained by digestion with chymotrypsin.
 CC GCAP-II is involved in insulin secretion by pancreatic beta cells. This
 CC peptide fragment could be used to which affects insulin secretion by the
 CC beta cells treat pancreatic endocrine disorders, especially diabetes
 CC mellitus type II, renal and intestinal disorders, disorders of the
 CC respiratory, gastrointestinal and urogenital apparatus, disorders of the
 CC cardiovascular and nervous systems, disorders of the integuments and
 CC sense organs and diseases associated with GCAP II (89-112) deficiency.
 CC This peptide can be used for treatment of electrolyte effects on bone
 CC reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP
 CC -II (89-112) can be used to treat diseases associated with overproduction
 CC of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP I (99-15) cDNA are
 CC useful for diagnosis and treatment of the above disorders e.g. gene
 CC therapy for diabetes
 XX Sequence 81 AA;
 Query Match 74.1%; Score 429; DB 2; Length 81;
 Best Local Similarity 100.0%; Pred. No. 2.4e-40;
 Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QGFRVQLSEMKKLSLEAQWAPSPRLQAQSLPVAVCHHPALPDQLQPVCAQSEASSI 91
 DB 1 QGFRVQLSEMKKLSLEAQWAPSPRLQAQSLPVAVCHHPALPDQLQPVCAQSEASSI 60
 QY 92 LRTIANDDCELCVNVACTGCL 112
 DB 61 LRTIANDDCELCVNVACTGCL 81

RESULT 11
 AAW23233
 ID AAW23233 standard; peptide; 81 AA.
 AC AAW23233;
 DT 29-OCT-1997 (first entry)
 XX GCAP-II C-terminal fragment prepared by chymotrypsin.
 KW Human; guanylate cyclase; activating peptide; GCAP-II; cGMP;
 KW transepithelial transport; treatment; kidney; intestinal; respiratory;
 KW urogenital; circulatory; nervous system; disorder; disease; endocrine;
 KW sensory; system; osteoporosis; dental; pancreas; diabetes; hypophysis;
 KW gastrointestinal tract; diarrhoea; gene therapy; probe;
 KW recombinant production; transgenic animal; antibody; immunoassay reagent.
 XX Homo sapiens.
 OS Homo sapiens.
 PN DE19528544-A1.
 PD 06-FEB-1997.
 XX 03-AUG-1995; 95DE-01028544.
 XX 03-AUG-1995; 95DE-01028544.
 PA (FORS/) FORSSMANN W.
 PI Forssmann W;
 XX WPI; 1997-110032/11.
 XX Guanylate cyclase activating peptide II - increases cGMP formation, and
 PT controls transport of water and electrolytes across epithelial cells.
 PS Claim 3; Page 6; 15pp; German.
 XX The present sequence is a carboxy-terminal fragment of the human
 CC guanylate cyclase activating peptide II (GCAP-II) precursor, prepared by
 CC endoproteolytic cleavage with chymotrypsin. GCAP-II increases cGMP
 CC formation, and is involved in the control of transepithelial water and
 CC electrolyte transport. GCAP-II can be used to treat a variety of kidney,
 CC intestinal, respiratory, urogenital, circulatory and nervous system
 CC disorders, diseases of the endocrine and sensory systems (e.g.
 CC osteoporosis, and dental disease), disorders of the pancreas (e.g.
 CC diabetes, and hypophysis) or the endocrine gastrointestinal tract and for
 CC the long term treatment of diarrhoea, without inducing an immune
 CC response. The GCAP-II cDNA can be used to treat the same conditions,
 CC clone the GCAP-II-encoding gene for use in gene therapy, as a
 CC hybridisation probe and for the production of recombinant GCAP-II or
 CC transgenic animal creation. Antibodies raised against GCAP-II are useful
 CC as immunoassay reagents. GCAP-II, or a fragment, are administered at,
 CC e.g. 100-1200 microg/day by intravenous or intramuscular injection or 300
 CC -1200 microg/day subcutaneously. They may also be given orally.
 CC intranasally or by inhalation, in typical unit doses of 0.3-30 mg. GCAP-
 CC II was chemically synthesised, or isolated by chromatography from T84
 CC transformed eukaryotic or prokaryotic cells, or human blood. When T84
 CC cells were incubated with synthetic GCAP-II, generation of cGMP production
 CC increased in a dose dependent manner. GCAP-II influences cGMP production
 CC via a known receptor for heat stable enterotoxin. Other stomach,
 CC intestinal, pancreatic and liver cells also responded to GCAP-II, e.g.
 CC via changes in intracellular Ca2+ ion concentration

XX Sequence 81 AA;
 SQ Query Match 74.1%; Score 429; DB 2; Length 81;
 Best Local Similarity 100.0%; Pred. No. 2.4e-40;
 Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 QGFRVQLESMMKSLDLEAQWAPSPRLQASLLPAVCHHPALPDQLQPVCAEQEASSIFKTLRT 91
 Db 1 QGFRVQLESMMKSLDLEAQWAPSPRLQASLLPAVCHHPALPDQLQPVCAEQEASSIFKTLRT 60
 Qy 92 LRTIANDDCELCVNVACTGCL 112
 Db 61 LRTIANDDCELCVNVACTGCL 81

RESULT 12
 AAW18486
 ID AAW18486 standard; peptide; 78 AA.
 XX AAW18486;
 AC
 XX
 DT 22-APR-1998 (first entry)
 XX Human GCAP-II (89-112) chymotrypsin digested fragment 3.
 DE
 XX Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic;
 KW diabetes; endocrine disorder; diagnosis; treatment; human.
 KW
 XX Homo sapiens.
 OS
 XX DE19543628-A1.
 PN
 XX 28-MAY-1997.
 PD
 XX 24-NOV-1995; 95DE-01043628.
 PF
 XX 24-NOV-1995; 95DE-01043628.
 PR
 XX (FORS/) FORSMANN W.
 PA
 XX Forsemann W, Kist A, Kruehoffer M, Meyer M, Pardigol A, Heine G;
 PI WPI; 1997-290350/27.
 XX
 XX New guanyl cyclase C activating peptide fragments - have insulinotropic
 PT activity, useful for treating diabetes, etc.
 PT
 XX Claim 3; Fig 3; 33pp; German.

XX Peptides AAW18484-W18487 represent fragments of the guanyl cyclase C
 CC activating peptide, GCAP-II, obtained by digestion with chymotrypsin.
 CC GCAP-II is involved in insulin secretion by pancreatic beta cells. This
 CC peptide fragment could be used to which affects insulin secretion by the
 CC beta cells treat pancreatic endocrine disorders, especially diabetes
 CC mellitus type II, renal and intestinal disorders, disorders of the
 CC respiratory, gastrointestinal and urogenital apparatus, disorders of the
 CC cardiovascular and nervous systems, disorders of the integuments and
 CC sense organs and diseases associated with GCAP II (89-112) deficiency.
 CC This peptide can be used for treatment of electrolyte effects on bone
 CC reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP
 CC -II (89-112) can be used to treat diseases associated with overproduction
 CC of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP I (99-15) cDNA are
 CC useful for diagnosis and treatment of the above disorders e.g. gene
 CC therapy for diabetes
 XX
 SQ Sequence 78 AA;
 Query Match 71.2%; Score 412; DB 2; Length 78;
 Best Local Similarity 100.0%; Pred. No. 1.9e-38;
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 RVQLESMMKSLDLEAQWAPSPRLQASLLPAVCHHPALPDQLQPVCAEQEASSIFKTLRT 94

Db 1 RVQLESMMKSLDLEAQWAPSPRLQASLLPAVCHHPALPDQLQPVCAEQEASSIFKTLRT 60
 Qy 95 IANDDCELCVNVACTGCL 112
 Db 61 IANDDCELCVNVACTGCL 78

RESULT 13
 AAW23234
 ID AAW23234 standard; peptide; 78 AA.
 XX AAW23234;
 AC
 XX
 DT 29-OCT-1997 (first entry)
 XX GCAP-II C-terminal fragment prepared by chymotrypsin.
 DE
 XX Human; guanylate cyclase; activating peptide; GCAP-II; cGMP;
 KW transepithelial transport; treatment; kidney; intestinal; respiratory;
 KW urogenital; circulatory; nervous system; disorder; disease; endocrine;
 KW sensory; system; osteoporosis; dental; pancreas; diabetes; hypophysis;
 KW gastrointestinal tract; diarrhoea; gene therapy; probe;
 KW recombinant production; transgenic animal; antibody; immunoassay reagent.
 XX
 OS Homo sapiens.
 XX DE19528544-A1.
 PN
 XX 06-FEB-1997.
 PD
 XX 03-AUG-1995; 95DE-01028544.
 PF
 XX 03-AUG-1995; 95DE-01028544.
 PR
 XX (FORS/) FORSMANN W.
 PA
 XX Forsemann W;
 PI WPI; 1997-110032/11.
 XX
 XX Guanylate cyclase activating peptide II - increases cGMP formation, and
 PT controls transport of water and electrolytes across epithelial cells.
 PT
 XX Claim 3; Page 6; 15pp; German.

XX The present sequence is a carboxy-terminal fragment of the human
 CC guanylate cyclase activating peptide II (GCAP-II) precursor, prepared by
 CC endoproteolytic cleavage with chymotrypsin. GCAP-II increases cGMP
 CC formation, and is involved in the control of transepithelial water and
 CC electrolyte transport. GCAP-II can be used to treat a variety of kidney,
 CC intestinal, respiratory, urogenital, circulatory and nervous system
 CC disorders, diseases of the endocrine and sensory systems (e.g.
 CC osteoporosis, and dental disease), disorders of the pancreas (e.g.
 CC diabetes, and hypophysis) or the endocrine gastrointestinal tract and for
 CC the long term treatment of diarrhoea, without inducing an immune
 CC response. The GCAP-II cDNA can be used to treat the same conditions,
 CC clone the GCAP-II-encoding gene for use in gene therapy, as a
 CC hybridisation probe and for the production of recombinant GCAP-II or
 CC transgenic animal creation. Antibodies raised against GCAP-II are useful
 CC as immunoassay reagents. GCAP-II, or a fragment, are administered at,
 CC e.g. 100-1200 microg/day by intravenous or intramuscular injection or 300
 CC -1200 microg/day subcutaneously. They may also be given orally.
 CC II was chemically synthesised, or isolated by chromatography from
 CC transformed eukaryotic or prokaryotic cells, or human blood. When T84
 CC cells were incubated with synthetic GCAP-II, generation of cGMP was
 CC increased in a dose dependent manner. GCAP-II influences cGMP production
 CC via a known receptor for heat stable enterotoxin. Other stomach,
 CC intestinal, pancreatic and liver cells also responded to GCAP-II, e.g.
 CC via changes in intracellular Ca²⁺ ion concentration
 XX
 SQ Sequence 78 AA;

Query Match 71.2%; Score 412; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.9e-38;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 RVQESMKKSLDLEAQWAPSPRLQASLLPAVCHHPALPDQLQPVCAQSEASSIFKTLRTI 94
DB 1 RVQESMKKSLDLEAQWAPSPRLQASLLPAVCHHPALPDQLQPVCAQSEASSIFKTLRTI 60

QY 95 IANDCELVCNVACTGCL 112
DB 61 IANDCELVCNVACTGCL 78

RESULT 14
AAW18468
ID AAW18468 standard; peptide; 77 AA.
AC AAW18468;
XX
DT 23-APR-1998 (first entry)
XX
DE Human GCAP-II (89-112) endoprotease Arg-C digested fragment 2.
XX
KW Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic;
KW diabetes; endocrine disorder; diagnosis; treatment; human.
XX
OS Homo sapiens.
XX
PN DE19543628-A1.
XX
PD 28-MAY-1997.
XX
PF 24-NOV-1995; 95DE-01043628.
XX
PR 24-NOV-1995; 95DE-01043628.
XX
PA (FORS/) FORSSMANN W.
XX
PI Forssmann W, Kist A, Kruhoeffner M, Meyer M, Pardigol A, Heine G;
XX
DR WPI; 1997-290350/27.
XX
PT New guanyl cyclase C activating peptide fragments - have insulinotropic
PT activity, useful for treating diabetes, etc.
XX
PS Claim 3; Fig 3; 33pp; German.
XX
CC Peptides AAW18467-W18470 represent fragments of the guanyl cyclase C
CC activating peptide, GCAP-II, obtained by digestion with endoprotease Arg-
CC C. GCAP-II is involved in insulin secretion by pancreatic beta cells.
CC This peptide fragment could be used to which affects insulin secretion by
CC the beta cells treat pancreatic endocrine disorders, especially diabetes
CC mellitus type II, renal and intestinal disorders, disorders of the
CC gastrointestinal, respiratory and urogenital apparatus, disorders of the
CC sense organs and diseases associated with GCAP II (89-112) deficiency.
CC This peptide can be used for treatment of electrolyte effects on bone
CC reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP
CC -II (89-112) can be used to treat diseases associated with overproduction
CC of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP I (99-15) cDNA are
CC useful for diagnosis and treatment of the above disorders e.g. gene
CC therapy for diabetes
XX
SQ Sequence 77 AA;

Query Match 70.3%; Score 407; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 6.7e-38;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 VQESMKKSLDLEAQWAPSPRLQASLLPAVCHHPALPDQLQPVCAQSEASSIFKTLRTI 95
DB 1 VQESMKKSLDLEAQWAPSPRLQASLLPAVCHHPALPDQLQPVCAQSEASSIFKTLRTI 60

Query Match 70.3%; Score 407; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 6.7e-38;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 VQESMKKSLDLEAQWAPSPRLQASLLPAVCHHPALPDQLQPVCAQSEASSIFKTLRTI 95
DB 1 VQESMKKSLDLEAQWAPSPRLQASLLPAVCHHPALPDQLQPVCAQSEASSIFKTLRTI 60

QY 96 ANDCELVCNVACTGCL 112
DB 61 ANDCELVCNVACTGCL 77

RESULT 15
AAW18479
ID AAW18479 standard; peptide; 77 AA.
XX
AC AAW18479;
XX
DT 22-APR-1998 (first entry)
XX
DE Human GCAP-II (89-112) trypsin digested fragment 2.
XX
KW Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic;
KW diabetes; endocrine disorder; diagnosis; treatment; human.
XX
OS Homo sapiens.
XX
PN DE19543628-A1.
XX
PD 28-MAY-1997.
XX
PF 24-NOV-1995; 95DE-01043628.
XX
PR 24-NOV-1995; 95DE-01043628.
XX
PA (FORS/) FORSSMANN W.
XX
PI Forssmann W, Kist A, Kruhoeffner M, Meyer M, Pardigol A, Heine G;
XX
DR WPI; 1997-290350/27.
XX
PT New guanyl cyclase C activating peptide fragments - have insulinotropic
PT activity, useful for treating diabetes, etc.
XX
PS Claim 3; Fig 3; 33pp; German.
XX
CC Peptides AAW18478-W18483 represent fragments of the guanyl cyclase C
CC activating peptide, GCAP-II, obtained by digestion with trypsin. GCAP-II
CC is involved in insulin secretion by pancreatic beta cells. This peptide
CC fragment could be used to which affects insulin secretion by the beta
CC cells treat pancreatic endocrine disorders, especially diabetes mellitus
CC type II, renal and intestinal disorders, disorders of the respiratory,
CC gastrointestinal and urogenital apparatus, disorders of the
CC cardiovascular and nervous systems, disorders of the integuments and
CC sense organs and diseases associated with GCAP II (89-112) deficiency.
CC This peptide can be used for treatment of electrolyte effects on bone
CC reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP
CC -II (89-112) can be used to treat diseases associated with overproduction
CC of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP I (99-15) cDNA are
CC useful for diagnosis and treatment of the above disorders e.g. gene
CC therapy for diabetes
XX
SQ Sequence 77 AA;

Query Match 70.3%; Score 407; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 6.7e-38;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 VQESMKKSLDLEAQWAPSPRLQASLLPAVCHHPALPDQLQPVCAQSEASSIFKTLRTI 95
DB 1 VQESMKKSLDLEAQWAPSPRLQASLLPAVCHHPALPDQLQPVCAQSEASSIFKTLRTI 60

QY 96 ANDCELVCNVACTGCL 112
DB 61 ANDCELVCNVACTGCL 77

Search completed: March 26, 2005, 16:44:28
Job time : 122.628 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:38:19 ; Search time 33.5182 Seconds
(without alignments)
249.437 Million cell updates/sec

Title: US-10-775-481A-56

Perfect score: 579

Sequence: 1 MGCRAAGLLPGVAVVLLLL.....RTIANDCELGVNACTGCL 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	162.5	28.1	115	2	US-07-903-029-4
2	162.5	28.1	115	2	US-07-903-029-5
3	133	23.0	115	2	US-07-903-029-6
4	96	16.6	16	1	US-08-145-940-1
5	96	16.6	16	2	US-08-583-447A-56
6	90	15.5	15	1	US-08-145-940-2
7	81	14.0	15	2	US-08-583-447A-55
8	80.5	13.9	1206	4	US-09-252-991A-19632
9	75	13.0	467	4	US-09-522-775A-4
10	74.5	12.9	623	4	US-09-949-016-7573
11	74.5	12.9	800	2	US-08-469-537A-72
12	74.5	12.9	800	2	US-08-469-537A-78
13	74.5	12.9	937	2	US-08-469-537A-105
14	73.5	12.7	208	4	US-09-328-352-4746
15	72	12.4	467	4	US-09-522-775A-2
16	72	12.4	475	4	US-09-949-016-10456
17	71.5	12.3	301	3	US-08-829-525-24
18	71.5	12.3	301	3	US-08-609-583A-24
19	71.5	12.3	301	3	US-08-937-399-24
20	71.5	12.3	301	4	US-09-310-367-24
21	71.5	12.3	301	4	US-09-032-337-24
22	71.5	12.3	301	4	US-09-464-231-24
23	71	12.3	88	4	US-09-252-991A-24612
24	71	12.3	260	4	US-09-252-991A-29887
25	69.5	12.0	309	4	US-09-489-039A-12224
26	69.5	12.0	350	4	US-09-270-767-58582
27	69.5	12.0	559	4	US-09-270-767-43239

28	69.5	12.0	934	4	US-09-949-016-7286	Sequence 7286, Ap
29	68.5	11.8	1046	4	US-09-489-039A-8148	Sequence 8148, Ap
30	68	11.7	242	4	US-09-059-625-74	Sequence 74, Appl
31	68	11.7	376	4	US-09-902-540-15516	Sequence 15516, A
32	67.5	11.7	680	4	US-09-949-016-10770	Sequence 10770, A
33	67.5	11.7	953	4	US-09-902-540-14681	Sequence 14681, A
34	67	11.6	475	4	US-09-252-991A-21041	Sequence 21041, A
35	66	11.4	376	4	US-09-270-767-42614	Sequence 42614, A
36	64.5	11.1	332	2	US-08-958-642-2	Sequence 2, Appli
37	64.5	11.1	332	3	US-08-778-394-4	Sequence 4, Appli
38	64.5	11.1	332	3	US-08-778-423A-2	Sequence 2, Appli
39	64.5	11.1	488	1	US-07-794-393-2	Sequence 2, Appli
40	64.5	11.1	488	1	US-08-001-711-2	Sequence 2, Appli
41	64.5	11.1	488	3	US-08-704-711A-22	Sequence 22, Appl
42	64.5	11.1	488	3	US-09-521-220-22	Sequence 22, Appl
43	64.5	11.1	488	3	US-09-391-104-31	Sequence 31, Appl
44	64.5	11.1	489	3	US-08-448-489-11	Sequence 11, Appl
45	64.5	11.1	489	4	US-09-689-730-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-07-903-029-4
; Sequence 4, Application US/07903029
; Patent No. 5969097
; GENERAL INFORMATION:
; APPLICANT: Wiegand, Roger C.
; APPLICANT: Currie, Mark C.
; TITLE OF INVENTION: Human Guanylin
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/903,029
; FILING DATE: 19920623
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: 07-21(872)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-5402
; TELEFAX: (314)694-9009
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-903-029-4

Query Match	28.1%;	Score	162.5;	DB 2;	Length	115;			
Best Local Similarity	36.1%;	Pred. No.	1.1e-12;						
Matches	35;	Conservative	15;	Mismatches	32;	Indels	15;	Gaps	3;
Qy	27	VTIQYQCFRVLQSMKKLSGLE-----AQWAPSRLQAGSLPAVCHHPALPDL	76						
Db	22	VTVDGNFSLSSVKKLKDLQEPQKPRVKLRNFAPIP---GEPVVILCSNPFPEEL	78						
Qy	77	QPVCAQSEASSIFKTLRTIAND--DCELCVNACTGC	111						

RESULT 4
US-08-145-940-1
; Sequence 1, Application US/08145940
; Patent No. 5489670
; GENERAL INFORMATION:
; APPLICANT: Curzie, Mark G.
; APPLICANT: Kita, Toshihiro
; APPLICANT: Smith, Christine E.
; APPLICANT: Fok, Kam F.
; TITLE OF INVENTION: Human Uroguanylin
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,940
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: 07-21 (808) A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 470-6501

TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-145-940-1

Query Match 16.6%; Score 96; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 NDCCLCVNVACTGCL 112
Db 1 NDCCLCVNVACTGCL 16

RESULT 5

US-08-583-447A-56
; Sequence 56, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-583-447A-56

Query Match 16.6%; Score 96; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 NDCCLCVNVACTGCL 112
Db 1 NDCCLCVNVACTGCL 16

RESULT 6

US-08-145-940-2

; Sequence 2, Application US/08145940
; Patent No. 5489670
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Kita, Toshihiro
; APPLICANT: Smith, Christine E.
; APPLICANT: Fok, Kam F.
; TITLE OF INVENTION: Human Uroguanylin
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,940
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: 07-21(808)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-145-940-2

Query Match 15.5%; Score 90; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 98 DDCELNVNACTGCL 112
Db 1 DDCELNVNACTGCL 15

RESULT 7

US-08-583-447A-55
; Sequence 55, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A

; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: T1U-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-583-447A-55

Query Match 14.0%; Score 81; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 0.0013;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 98 DCELCNVNACTGC 111
DB 2 EDCELCNVACTGC 15
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RESULT 8

US-09-252-991A-19632
; Sequence 19632, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19632
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19632

Query Match 13.9%; Score 80.5; DB 4; Length 1206;
Best Local Similarity 36.5%; Pred. No. 0.68;
Matches 27; Conservative 6; Mismatches 34; Indels 7; Gaps 3;

QY 33 GFRVQLESKKUSDLRAQWAPSRLOAQSLIPAVCHHPALPDLOPVCAOSEASSIFKTL 92
DB 853 GFSLOAEGGFKLADPQLAWRP---LQGWRLPTVLHAPPA---DLFG-CGHYRVIQPFSTL 905
QY 93 RTIANDDCELCNVN 106
DB 906 RESASIDGALSTGL 919

RESULT 9

US-09-522-775A-4
; Sequence 4, Application US/09522775A
; Patent No. 6660906
; GENERAL INFORMATION:
; APPLICANT: Tschalis, Philip N.
; TITLE OF INVENTION: Inhibition of Tpl2 To Treat Inflammatory Diseases
; FILE REFERENCE: OTT-3202

; CURRENT APPLICATION NUMBER: US/09/522,775A
; CURRENT FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Rat Tpl2 polypeptide sequence
US-09-522-775A-4

Query Match 13.0%; Score 75; DB 4; Length 467;
Best Local Similarity 33.3%; Pred. No. 0.9;
Matches 25; Conservative 15; Mismatches 25; Indels 10; Gaps 4;

QY 41 MKKLSLEAQWAPSRLOAQSLIPAVCHHPAL--PDLOPVCAOSEASSIFKTLRTIAND 98
DB 361 MRELIEAALERNPNHRPKAADLL---KHEALNPREDQPCQSILD-SALFDRKLLSRK 415
QY 99 DCELCNVNVA---CTG 110
DB 416 ELEPENIADSSCTG 430
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RESULT 10

US-09-949-016-7573
; Sequence 7573, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7573
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7573

Query Match 12.9%; Score 74.5; DB 4; Length 623;
Best Local Similarity 24.1%; Pred. No. 1.6;
Matches 26; Conservative 20; Mismatches 29; Indels 33; Gaps 6;

QY 12 GVAVVLLLLLOSTQSVYIQGFRVQLES-----KKLSLEAQWAPSRLOAQ 60
DB 144 GIACARFI---GNRTVWESLHMQGEIENQITAAFTWIGTSSLSDKCSQFA----- 192
QY 61 SLLPAVCHHPALPDLOPVCAOSEASSIFKTLRTIANDDCELCNVNAC 108
DB 193 --IFSLCHYAF-----PYC--DETSSVPKP-RDLCRDECEILENVLC 229
:|||||:|||||

RESULT 11

US-08-469-537A-72
; Sequence 72, Application US/08469537A
; Patent No. 5843749
; GENERAL INFORMATION:
; APPLICANT: Maisonnier, et al.
; TITLE OF INVENTION: EHK AND ROR TYROSINE
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:

; NAME: Kempler, Ph.D., Gail M
 ; REGISTRATION NUMBER: 32,143
 ; REFERENCE/DOCKET NUMBER: REG 070C
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 914-345-7400
 ; TELEFAX: 914-345-7721
 ; TELEX:

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; INFORMATION FOR SEQ ID NO: 105:
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; SEQUENCE CHARACTERISTICS:
;     LENGTH: 937 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;
;     MOLECULE TYPE: protein
;     FRAGMENT TYPE: internal
;     FEATURE:
;
;     NAME/KEY: Human RORI
;     LOCATION: 1..937
;     OTHER INFORMATION:
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US-08-469-537A-105

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RESULT 14

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US-09-328-352-4746
; Sequence 4746, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4746
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4746

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RESULT 15

RESOL. 15
US-09-522-775A-2
; Sequence 2, Application US/09522775A
; Patent No. 660906
; GENERAL INFORMATION:
; APPLICANT: Tschlis, Philip N.
; TITLE OF INVENTION: Inhibition of Tpl2 To Treat Inflammatory Diseases
; FILE REFERENCE: OTT-3202

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:48:40 ; Search time 111.591 Seconds
(without alignments)
332.314 Million cell updates/sec

Title: US-10-775-481A-56
Perfect score: 579
Sequence: 1 MGCRAASGLPGVAVVLLLL.....RTIANDDCELCVNVACTGCL 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	100.0	112	17	US-10-479-606-5
2	252	43.5	109	17	US-10-479-606-6
3	216	37.3	85	9	US-09-925-299-1527
4	216	37.3	85	10	US-09-925-299-1527
5	162.5	28.1	115	9	US-09-981-353-61
6	162.5	28.1	115	14	US-10-235-994-22
7	162.5	28.1	115	14	US-10-262-473-12
8	162.5	28.1	115	17	US-10-479-606-4
9	136	23.5	108	14	US-10-262-473-16
10	132	22.8	102	14	US-10-262-473-14
11	96	16.6	16	14	US-10-107-814-1
12	96	16.6	16	14	US-10-197-954-141
13	96	16.6	16	15	US-10-621-684-56
Sequence 5, Appli					
Sequence 6, Appli					
Sequence 1527, Ap					
Sequence 1527, Ap					
Sequence 61, Appli					
Sequence 22, Appli					
Sequence 12, Appli					
Sequence 4, Appli					
Sequence 16, Appli					
Sequence 14, Appli					
Sequence 141, App					
Sequence 56, Appli					

ALIGNMENTS

RESULT 1

US-10-479-606-5
; Sequence 5, Application US/10479606
; Publication No. US20050032684A1
; GENERAL INFORMATION:
; APPLICANT: Savas, Yulsel
; TITLE OF INVENTION: Guanylate-cyclase C ligand, administered via the airways, for the treatment of respiratory airway problems
; FILE REFERENCE: 03100192aa
; CURRENT APPLICATION NUMBER: US/10/479,606
; PRIOR FILING DATE: 2003-12-04
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/DE02/02040
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 112
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-479-606-5

Query Match 100.0%; Score 579; DB 17; Length 112;
Best Local Similarity 100.0%; Pred. No. 8.2e-59;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGCRAASGLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKKLSDLLEAOWAPSPRLQAQ 60

Db 1 MGCRAASGLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKKLSDLLEAOWAPSPRLQAQ 60

Qy 61 SLLPACVCHHPALPDQLQPVCAQSQASISFKTLRTIANDDCELCVNVACTGCL 112

Db 61 SLLPACVCHHPALPDQLQPVCAQSQASISFKTLRTIANDDCELCVNVACTGCL 112

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RESULT 2
US-10-479-606-6
; Sequence 6, Application US/10479606
; Publication No. US20050032684A1
; GENERAL INFORMATION:
; APPLICANT: Cetin, Yalcin
; APPLICANT: Savas, Yuksel
; TITLE OF INVENTION: Guanylate-cyclase C ligand, administered via the airways, for the
; FILE REFERENCE: 03100192aa
; CURRENT APPLICATION NUMBER: US/10/479,606
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: DE10127119.0
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/DE02/02040
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: opossum
US-10-479-606-6

Query Match 43.5%; Score 252; DB 17; Length 109;
Best Local Similarity 50.5%; Pred. No. 4.9e-21;
Matches 52; Conservative 17; Mismatches 32; Indels 2; Gaps 2;

Qy 10 LP-GVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLBAQWAPSPRLQAQSLPAV-C 67
Db 6 LPMAVTAMLLTIAQNTQSVYIQGFRVQLESMMKLSDLBAQWAPSPRLQAQSLPAV-C 65
Qy 68 HHPALPDLPQVCASQASISFTKLTITANDCCLCVNACTG 110
Db 66 SDPALPSDLPVCENSQAVNIFRALRYINQEBCELCINMACTG 108

RESULT 3
US-09-925-299-1527
; Sequence 1527, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1527
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (28)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (29)
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (31)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (32)
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; NAME/KEY: SITE
; LOCATION: (34)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (38)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (39)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (42)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (43)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (47)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (52)
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; NAME/KEY: SITE
; LOCATION: (53)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (55)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (66)
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; NAME/KEY: SITE
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; NAME/KEY: SITE
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; LOCATION: (83)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1527
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Query Match 37.3%; Score 216; DB 9; Length 85;
Best Local Similarity 62.5%; Pred. No. 5.1e-17;
Matches 45; Conservative 3; Mismatches 24; Indels 0; Gaps 0;
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Qy 1 MGCRAASGLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSDLBAQWAPSPRLQAQ 60
Db 11 MGCWVASGLLTGLAEVLXXLXXTXQGXKQYXXFRVXLESMMKLSDLBAQWAPSPXLEAX 70
Qy 61 SLLPAVCHHPAL 72
Db 71 XLLAAVCHHPAL 82
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RESULT 4
US-09-925-299-1527
; Sequence 1527, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
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: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA102
: CURRENT APPLICATION NUMBER: US/09/925,299
: CURRENT FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05883
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 1556
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 1527
: LENGTH: 85
: TYPE: PRP
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (1)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (3)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (9)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
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: NAME/KEY: SITE
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: NAME/KEY: SITE
: LOCATION: (52)
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: LOCATION: (55)
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: LOCATION: (60)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (66)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE

```

```

US/10/235-994-22
; Sequence 22, Application US/10235994
; Publication No. US20030101002A1
; GENERAL INFORMATION:
; APPLICANT: Bartha, Gabor
; APPLICANT: Walker, Michael
; TITLE OF INVENTION: METHODS FOR ANALYZING GENE EXPRESSION PATTERNS
; FILE REFERENCE: ICYP012
; CURRENT APPLICATION NUMBER: US/10/235,994
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US/10/003,608
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,081
; PRIOR FILING DATE: 2000-11-01

```


Best Local Similarity 36.0%; Pred. No. 1.2e-07;
Matches 32; Conservative 15; Mismatches 32; Indels 10; Gaps 4;
Qy 27 VYIQGFRVLE-SMKKLSLEAQWAPSPRLQAQSLLPVACHHPALPDQLQPVCAQSEA 85
Db 25 VTVDQGNFSFSLPRVGLRN----FAPIP---GEPVVPILCSNPFPEELKPLCKEPNA 77
Qy 86 SSIFKTLRTIAND--DCELCNVNACTGCL 112
Db 78 QEILQRLIEIAEDPGTCEICAYAACTGCL 106
RESULT 10
US-10-262-473-14
; Sequence 14, Application US/10262473
; Publication No. US20030199442A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John,
; APPLICANT: Burgess, Catherine,
; APPLICANT: Gorman, Linda,
; APPLICANT: Guo, Xiaojia,
; APPLICANT: Lepley, Denise,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rastelli, Luca,
; APPLICANT: Reiger, Daniel,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-462B
; CURRENT APPLICATION NUMBER: US/10/262,473
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Curasequid version 0.1
; SEQ ID NO 14
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-473-14
Query Match 22.8%; Score 132; DB 14; Length 102;
Best Local Similarity 35.2%; Pred. No. 3.3e-07;
Matches 31; Conservative 15; Mismatches 32; Indels 10; Gaps 4;
Qy 27 VYIQGFRVLE-SMKKLSLEAQWAPSPRLQAQSLLPVACHHPALPDQLQPVCAQSEA 85
Db 22 VTVDQGNFSFSLPRVGLRN----FAPIP---GEPVVPILCSNPFPEELKPLCKEPNA 74
Qy 86 SSIFKTLRTIAND--DCELCNVNACTGCL 111
Db 75 QEILQRLIEIAEDPGTCEICAYAACTGCL 102
RESULT 11
US-10-107-814-1
; Sequence 1, Application US/10107814
; Publication No. US20030073628A1
; GENERAL INFORMATION:
; APPLICANT: SHAILUBHAI, KUNWAR
; APPLICANT: NIKIFOROVICH, GREGORY
; APPLICANT: JACOB, GARY S.
; TITLE OF INVENTION: GUANYLATE CYCLASE RECEPTOR AGONISTS FOR THE TREATMENT
; TITLE OF INVENTION: OF TISSUE INFLAMMATION AND CARCINOGENESIS
; FILE REFERENCE: 81361/284943/MAS

CURRENT APPLICATION NUMBER: US/10/107,814
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: DISULFID
LOCATION: (4)..(12)
NAME/KEY: DISULFID
LOCATION: (7)..(15)
US-10-107-814-1
Query Match 16.6%; Score 96; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 97 NDDCELCNVNACTGCL 112
Db 1 NDDCELCNVNACTGCL 16
RESULT 12
US-10-197-954-141
; Sequence 141, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K'ster, Hubert
; APPLICANT: Siddiqi, Suhail
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-197-954-141
Query Match 16.6%; Score 96; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 97 NDDCELCNVNACTGCL 112
Db 1 NDDCELCNVNACTGCL 16
RESULT 13
US-10-621-684-56
; Sequence 56, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor

CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,694
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-621-684-56

Query Match 16.6%; Score 96; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 NDDCELCVNVACTGCL 112
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DB 1 NDDCELCVNVACTGCL 16

RESULT 14

US-10-479-606-2
Sequence 2, Application US/10479606
Publication No. US20050032684A1
GENERAL INFORMATION:
APPLICANT: Savas, Yuxsel
TITLE OF INVENTION: Guanylate-cyclase C ligand, administered via the airways, for the
FILE REFERENCE: 03100192aa
CURRENT APPLICATION NUMBER: US/10/479,606
CURRENT FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: DE10127119.0
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/DE02/02040
PRIOR FILING DATE: 2002-06-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-10-479-606-2

Query Match 16.6%; Score 96; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 NDDCELCVNVACTGCL 112
|||||

DB 1 NDDCELCVNVACTGCL 16

RESULT 15

US-10-760-085-141
Sequence 141, Application US/10760085
Publication No. US20050042771A1
GENERAL INFORMATION:
APPLICANT: Hubert K'water
APPLICANT: Daniel Paul Little
APPLICANT: Suhaib Mahmood Siddiqi
APPLICANT: Matthew Peter Grealish
APPLICANT: Subramaniam Marappan
APPLICANT: Chester Frederick Hassman III
APPLICANT: Ping Yip
TITLE OF INVENTION: Capture Compounds, Collections Thereof
TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
FILE REFERENCE: 24743-2309
CURRENT APPLICATION NUMBER: US/10/760,085
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: 60/441,398
PRIOR FILING DATE: 2003-01-16
NUMBER OF SEQ ID NOS: 149
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 141
LENGTH: 16
TYPE: PRT
ORGANISM: Homo Sapien
US-10-760-085-141

Query Match 16.6%; Score 96; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 NDDCELCVNVACTGCL 112
|||||
DB 1 NDDCELCVNVACTGCL 16

Search completed: March 26, 2005, 17:16:38
Job time : 111.591 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:37:49 ; Search time 23.708 Seconds
(without alignments)
454.541 Million cell updates/sec

Title: US-10-775-481A-56
Perfect score: 579
Sequence: 1 MGCRAASGLPGVAVVLLLL.....RTIANDDCELCVNVACTGCL 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	579	100.0	112	2 JC4651	uroguanylin precursor
2	162.5	28.1	115	1 A46279	guanylylin precursor
3	161	27.8	116	2 JC7620	guanylin precursor
4	153.5	26.5	116	1 B46279	guanylin precursor
5	133	23.0	115	1 JN0318	guanylin precursor
6	81	14.0	72	1 QHEC1B	heat-stable entero
7	76.5	13.2	500	2 B86312	type 2A protein se
8	75	13.0	467	2 A47388	serine/threonine p
9	74.5	12.9	937	2 A45082	neurotrophic recep
10	74	12.8	72	1 QHEC4	heat-stable entero
11	74	12.8	467	2 I49609	proto-oncogene pro
12	74	12.8	824	2 I50618	C-fps proto oncoge
13	72	12.4	467	2 A48713	serine/threonine-s
14	71	12.3	737	2 S63453	probable RNA helic
15	68.5	11.8	369	2 AG0386	S-amino-6-(5-phosp
16	68.5	11.8	699	2 T18984	hypothetical prote
17	68	11.7	873	1 TVFVFS	protein-tyrosine k
18	66.5	11.5	538	2 AC1850	NADH dehydrogenase
19	66.5	11.5	1127	2 T21635	hypothetical prote
20	66.5	11.5	1165	2 T21636	hypothetical prote
21	66	11.4	580	2 T43485	hypothetical prote
22	65.5	11.3	144	2 C70937	hypothetical prote
23	65.5	11.3	322	2 D86760	phosphate starvati
24	65.5	11.3	533	1 TVFVFP	protein-tyrosine k
25	65	11.2	710	2 T52573	cyclic nucleotide
26	64.5	11.1	211	2 D82109	outer membrane lip
27	64.5	11.1	367	2 F82098	riboflavin-specifi
28	64.5	11.1	378	2 B99588	protein R09F10.7 [
29	64.5	11.1	488	2 S13423	stromelysin 3 (BC

30	64.5	11.1	1736	2 T00391	hypothetical prote
31	64	11.1	344	2 T12307	NADH2 dehydrogenas
32	64	11.1	456	2 A31857	ribonuclease inhib
33	64	11.1	465	2 S41644	polyadenylate-bind
34	64	11.1	537	2 T28683	hypothetical prote
35	64	11.1	614	1 I48385	RNA helicase TN22
36	64	11.1	1040	2 AD0771	probable RND-famil
37	63.5	11.0	349	2 JC5827	paired-box contain
38	63.5	11.0	445	2 T50005	hypothetical prote
39	63.5	11.0	589	2 T29895	hypothetical prote
40	63.5	11.0	707	2 T40070	origin recognition
41	63.5	11.0	848	2 S24981	adenylate cyclase
42	63.5	11.0	1088	2 H96747	unknown protein T1
43	63	10.9	96	2 A27166	ribosomal protein
44	63	10.9	692	2 E90952	flagellar biosynth
45	63	10.9	692	2 A85801	flagellar biosynth

ALIGNMENTS

RESULT 1

JC4651
uroguanylin precursor - human
N:Alternate names: guanylyl cyclase activating peptide II
C:Species: Homo sapiens (man)
C:Date: 10-May-1996 #sequence revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: JC4651; S63702; S68052
R:Miyazato, M.; Nakazato, M.; Yamaguchi, H.; Date, Y.; Kojima, M.; Kangawa, K.; Matsuo, Biochem. Biophys. Res. Commun. 219, 644-648, 1996
A:Title: Cloning and characterization of a cDNA encoding a precursor for human uroguanylin
A:Reference number: JC4651; MUID:96193705; PMID:8605041
A:Accession: JC4651
A:Molecule type: mRNA
A:Residues: 1-112 <MY>
A:Cross-references: UNIPROT:Q16661; GB:U34279; NID:gl236798; PIDN:AA050416.1; PID:gl2367
R:Hill, O.; Cetin, Y.; Cieslak, A.; Maegert, H.J.; Forssmann, W.G.
Biochim. Biophys. Acta 1253, 146-149, 1995
A:Title: A new human guanylate cyclase-activating peptide (GCAP-II, uroguanylin): precursor
A:Reference number: S63702; MUID:96106424; PMID:8519795
A:Accession: S63702
A:Molecule type: mRNA
A:Residues: 1-112 <HIL>
A:Cross-references: EMBL:Z50753; NID:g974823; PIDN:CAA90629.1; PID:g974824
R:Hess, R.; Kuhn, M.; Schulz-Knappe, P.; Raida, M.; Fuchs, M.; Klodt, J.; Adermann, K.; FEBS Lett. 374, 34-38, 1995
A:Title: GCAP-II: isolation and characterization of the circulating form of human urogu
A:Reference number: S68052; MUID:96049550; PMID:7589507
A:Accession: S68052
A:Molecule type: protein
A:Residues: 89-99,'X',101-102,'X',104-107,'X',109-110,'X',112 <HES>
C:Comment: This protein, a member of the guanylin peptide family, is an endogenous activ

C:Superfamily: Guanylin
C:Keywords: intestine
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-112/Product: uroguanylin #status predicted <WAT>

Query Match 100.0%; Score 579; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.1e-54;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGCRAASGLPGVAVVLLLLLQSTQSVYIQGFRVQLESMMKLSLEAOWAPSPRLQAQ	60
Db	1	MGCRAASGLPGVAVVLLLLLQSTQSVYIQGFRVQLESMMKLSLEAOWAPSPRLQAQ	60
Qy	61	SLPAPVCHHPALPDQLQPVCAQSEASSIFKTLRTIANDDCELCVNVACTGCL	112
Db	61	SLPAPVCHHPALPDQLQPVCAQSEASSIFKTLRTIANDDCELCVNVACTGCL	112

RESULT 2

A46279
 guanylin precursor [validated] - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Sep-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C:Accession: A46279; S29228; S29807
 R:De Sauvage, F.J.; Keshav, S.; Kuang, W.J.; Gillett, N.; Henzel, W.; Goeddel, D.V.
 Proc. Natl. Acad. Sci. U.S.A. 89, 9089-9093, 1992
 A>Title: Precursor structure, expression, and tissue distribution of human guanylin.
 A:Reference number: A46279; MUID:93028409; PMID:1409606
 A:Accession: A46279
 A:Molecule type: mRNA
 A:Residues: 1-115 <DEI>
 A:Cross-references: UNIPROT:Q02747; GB:M95174; NID:g306823; PIDN:AAA58625.1; PID:g306824
 R:Wiegand, R.C.; Kato, J.; Huang, M.D.; Pok, K.F.; Kachur, J.F.; Currie, M.G.
 PNAS Lett. 311, 150-154, 1992
 A>Title: Human guanylin: cDNA isolation, structure, and activity.
 A:Reference number: S29228; MUID:93011964; PMID:1327879
 A:Accession: S29228
 A:Molecule type: mRNA
 A:Residues: 1-115 <WIE>
 A:Cross-references: GB:M97496; NID:g183414; PIDN:AAA35915.1; PID:g183415
 R:Kuhn, M.; Raiba, M.; Adernann, K.; Schulz-Knappe, P.; Gerzer, R.; Heim, J.M.; Forssman
 FEBS Lett. 318, 205-209, 1993
 A>Title: The circulating bioactive form of human guanylin is a high molecular weight peptide.
 A:Reference number: S29807; MUID:93178628; PMID:8095028
 A:Accession: S29807
 A:Molecule type: protein
 A:Residues: 22-68 <KUH>
 A:Experimental source: plasma
 A:Note: amino-terminal sequencing of mature form and molecular weight of mature form by n of the same receptor.
 C:Genetics:
 A:Gene: GDB:GUCA2
 A:Cross-references: GDB:136460; OMIM:139392
 A:Map position: lp35-1p34
 C:Superfamily: guanylin
 C:Keywords: hormone; intestine
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-115/Product: guanylin #status experimental <MAT>
 Query Match 28.1%; Score 162.5; DB 1; Length 115;
 Best Local Similarity 36.1%; Pred. No. 5.3e-10;
 Matches 35; Conservative 15; Mismatches 32; Indels 15; Gaps 3;
 QY 27 VYIQGFRVQLSMKLSLE-----AQWAPSPRLQASLLPAVCHHPALPQDL 76
 DB 22 VTVDGNFSLSVSKKLDQEPQPRVGLKRNFAPIP---GEPVVPILCSNPFPPEL 78
 QY 77 QPVCAQEAASSIFKTLRTIAND--DCELCVNVACTGC 111
 DB 79 KPLCKEPNAQEIQLRLEEAEDPGTCEICAYACTGC 115
 RESULT 3
 JN0318
 guanylin precursor, long form - European eel
 C:Species: Anguilla anguilla (European eel)
 C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
 C:Accession: JC7620
 R:Comrie, M.M.; Cutler, C.P.; Cramb, G.
 Biochem. Biophys. Res. Commun. 281, 1078-1085, 2001
 A>Title: Cloning and expression of guanylin from the European eel (Anguilla anguilla).
 A:Reference number: JC7620; MUID:21139737; PMID:11243845
 A:Accession: JC7620
 A:Molecule type: mRNA
 A:Residues: 1-116 <COM>
 A:Cross-references: GB:AJ301673
 C:Comment: This protein, a member of a family of heat-stable peptides, is a potent extra axis. This peptide signalling system plays a role in osmoregulation in euryhaline teleosts.
 C:Superfamily: guanylin
 C:Keywords: heat-stable protein; osmoregulation

F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-116/Product: guanylin precursor, long form #status predicted <MAT>
 F:33-39/Region: homologous #status predicted
 F:69-114/Region: highly conserved #status predicted
 Query Match 27.8%; Score 161; DB 2; Length 116;
 Best Local Similarity 39.4%; Pred. No. 7.7e-10;
 Matches 43; Conservative 13; Mismatches 39; Indels 14; Gaps 4;
 QY 14 AVVLLLL-----LQSTQSVYIQGFRVQLSMKLSLEAQWAPS-----PRLOAQSLP 65
 DB 12 AVVLLLLAFCFLQESGVVMDGLISFPLEAVKVLKHLGANTMTSPHPNGLSH-----A 67
 QY 66 VCHHPALPDOLPVCASQASIFKTLRTIAN--DCELCVNVACTGC 112
 DB 68 VCSNPLHPAFLPVCEREGASALFNRLVDIITPPDPCEICANACTGC 116
 RESULT 4
 B46279
 guanylin precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 22-Sep-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C:Accession: A55643; B46279
 R:Sciaky, D.; Kosiba, J.L.; Cohen, M.B.
 Genomics 24, 583-587, 1994
 A>Title: Genomic sequence of the murine guanylin gene.
 A:Reference number: A55643; MUID:95229161; PMID:7713512
 A:Accession: A55643
 A:Molecule type: DNA
 A:Residues: 1-116 <SCI>
 A:Cross-references: UNIPROT:P33680; GB:U60528; GB:U09741; NID:g1480667; PIDN:AA05758.1; R:de Sauvage, F.J.; Keshav, S.; Kuang, W.J.; Gillett, N.; Henzel, W.; Goeddel, D.V.
 Proc. Natl. Acad. Sci. U.S.A. 89, 9089-9093, 1992
 A>Title: Precursor structure, expression, and tissue distribution of human guanylin.
 A:Reference number: A46279; MUID:93028409; PMID:1409606
 A:Accession: B46279
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-116 <DEI>
 A:Cross-references: GB:M95175; NID:g309282; PIDN:AAA37758.1; PID:g309283
 A:Note: sequence extracted from NCBI backbone (NCBI:P115379)
 C:Comment: Guanylin is an endogenous ligand for an intestine-specific receptor guanylyl n of the same receptor.
 C:Genetics:
 A:Introns: 25/3; 96/1
 C:Superfamily: guanylin
 C:Keywords: hormone; intestine
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-116/Product: guanylin #status predicted <MAT>
 Query Match 26.5%; Score 153.5; DB 1; Length 116;
 Best Local Similarity 36.8%; Pred. No. 4.8e-09;
 Matches 42; Conservative 13; Mismatches 40; Indels 19; Gaps 5;
 QY 9 LLPGVAVVLLLLQSTQSVYIQGFRVQLSMKLSLEAQWAP-----SPRLQAO 60
 DB 11 LLGALAVLV-----EGTVVDGLSFPLESVKKLGKLEVOEPRLVSHKXKAPRL-LQ 62
 QY 61 SLLPAVC-HHPALPDOLPVCASQEAASSIFKTLRTIAND--DCELCVNVACTGC 111
 DB 63 PVAPQLCSSHSALEALRPVCEKPNABEIIQLRLEAIAQDPNTEICAYACTGC 116
 RESULT 5
 JN0318
 guanylin precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 04-Dec-1992 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C:Accession: JN0318; A43345; A38194; S25489
 R:Wiegand, R.C.; Kato, J.; Currie, M.G.
 Biochem. Biophys. Res. Commun. 185, 812-817, 1992
 A>Title: Rat guanylin cDNA: characterization of the precursor of an endogenous activator

[illegible]

RESULT 8

A47388
serine/threonine protein kinase - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A47388
R:Patriotis, C.; Makris, A.; Bear, S.E.; Tschlis, P.N.
Proc. Natl. Acad. Sci. U.S.A. 90, 2251-2255, 1993
A>Title: Tumor progression locus 2 (Tpl-2) encodes a protein kinase involved in the pro
A/Reference number: A47388; MUID:93211939; PMID:7681591
A:Accession: A47388
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-467 <P>
A:Cross-references: UNIPROT:Q63562; GB:M94454; NID:g207082; PIDN:AAA42185.1; PID:g207083
A:Experimental source: liver
A>Note: sequence extracted from NCBI backbone (NCBIN:128133, NCBIP:128134)
F:136-388/Domain: protein kinase homology <KIN>

Query Match 13.0%; Score 75; DB 2; Length 467;
Best Local Similarity 33.3%; Pred. No. 4.3;
Matches 25; Conservative 15; Mismatches 25; Indels 10; Gaps 4;

QY 41 MKKLSDLEAQWAPSPRLQAQSLLPAVCHHPAL--PDQLQPVCAQSEASSIFKTTLRTIAND 98
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db 361 MRELIEAALERNPHRPKAADLL----KHEALNPREDQPCOSLD-SALFDKRLLSRK 415
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
QY 99 DCELCNVVA---CTG 110
|::||::||::||
Db 416 ELELPENIADSCTG 430
|::||::||::||

RESULT 9

A45082
Neurotrophic receptor rorl precursor - human
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: A45082
R:Masiaowski, P.; Carroll, R.D.
J. Biol. Chem. 267, 26181-26190, 1992
A>Title: A novel family of cell surface receptors with tyrosine kinase-like domain.
A/Reference number: A45082; MUID:93100347; PMID:1334494
A:Accession: A45082
A:Molecule type: mRNA
A:Residues: 1-937 <MAS>
A:Cross-references: UNIPROT:Q01973; GB:M97675; NID:g337464; PIDN:AAA60275.1; PID:g337465
A>Note: sequence extracted from NCBI backbone (NCBIP:120916)
C:Genetics:
A:Gene: GDB:NTRKR1
A:Cross-references: GDB:I136453
A:Map position: gp21-gp21
C:Superfamily: neurotrophic receptor ror; immunoglobulin homology; kringle homology; pro
F:Keywords: ATP; glycoprotein; kringle; phosphotransferase; transmembrane protein; tyro
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-937/Product: neurotrophic receptor rorl #status predicted <MAT>
F:72-133/Domain: immunoglobulin homology <IMM>
F:313-391/Domain: kringle homology <KRG>
F:404-425/Domain: transmembrane #status predicted <TM1>
F:471-753/Domain: protein kinase homology <KIN>
F:47,66,184,315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.9%; Score 74.5; DB 2; Length 937;
Best Local Similarity 24.1%; Pred. No. 10;
Matches 26; Conservative 20; Mismatches 29; Indels 33; Gaps 6;

QY 12 GVAVLLLLLQSTQSVYIQGFPRVQLESM-----KKLSDLAEQWAPSPRLQAQ 60
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db 175 GIACARFI---GNRTVMESLHWQEINQITAAFTMTGTSSHSLDKCSQA----- 223
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
QY 61 SLTPAVCHHPALPDQLQPVCAQSEASSIFKTTLRTIANDCELCNVAV 108
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

RESULT 12
I50618
C:fps proto oncogene - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50618
R:Huang, C.C.; Hammond, C.; Bishop, J.M.
J. Mol. Biol. 181, 175-186, 1985
A:Title: Nucleotide sequence and topography of chicken c-fps. Genesis of a retroviral on
A:Reference number: I50618; MUID:85160839; PMID:3879969
A:Accession: I50618
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-824 <HUA>
A:Cross-references: UNIPROT:Q90778; EMBL:X02266; NID:G63203; PIDN:CAA26155.1; PID:g87104
C:Genetics:
A:Gene: c-fps
A:Introns: 75/3; 133/3; 166/1; 227/2; 273/2; 313/2; 354/2; 416/3; 442/3; 512/3; 553/3; 5
C:Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology
C:Keywords: ATP
F:462-547/Domain: SH2 homology <SH2>
F:561-823/Domain: protein kinase homology <KIN>
F:569-577/Region: protein kinase ATP-binding motif

Query Match 12.8%; Score 74; DB 2; Length 824;
Best Local Similarity 29.3%; Pred. No. 10;
Matches 29; Conservative 13; Mismatches 31; Indels 26; Gaps 4;
Molecules type: DNA

Qy 9 LLPGVAVVLLLLQSTQSVYIQYQGF---RVQLSEMK-----KLSDLAEAWAPSPRLQAO 60
Db 349 LSPGERVHLLKRGQLQQAQQLQGLVCAQAKLQARDMLAKLAELGSEPP----- 401

Qy 61 SLLPAVCHHPALP--QDLQPVCAQOEASSIFKTLRTIAN 97
Db 402 -----PALPQEDRQSVCTDQERSGVTALETIKN 431

RESULT 13
A48713
serine/threonine-specific protein kinase cot, 58K form - human
N:Alternate names: cot proto-oncogene, 58K form
N:Contains: serine/threonine-specific protein kinase cot, 52K form
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A48713; B48713; S31639
R:Aoki, M.; Hamada, F.; Sugimoto, T.; Sumida, S.; Akiyama, T.; Toyoshima, K.
J. Biol. Chem. 268, 22723-22732, 1993
A:Title: The human cot proto-oncogene encodes two protein serine/threonine kinases with
A:Reference number: A48713; MUID:94043034; PMID:8226782
A:Accession: A48713
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-467 <AOK>
A:Cross-references: UNIPROT:P41279
A:Experimental source: TCO-4 cells
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:138970, NCBI:P:138971)
A:Accession: B48713
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 30-467 <AO2>
A:Experimental source: TCO-4 cells
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:138970, NCBI:P:138972)
R:Chan, A.M.; Chedid, M.; Aaronson, S.A.; Mikki, T.; McGovern, E.S.
Submitted to the EMBL Data Library, July 1992
A:Description: A transforming gene isolated by expression cloning from Ewing's sarcoma c
A:Reference number: S31639
A:Accession: S31639
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-467 <CHA>

A:Cross-references: EMBL:Z14138; NID:g31244; PIDN:CAA78512.1; PID:g31245
C:Keywords: alternative initiators; proto-oncogene
F:136-388/Domain: protein kinase homology <KIN>

Query Match 12.4%; Score 72; DB 2; Length 467;
Best Local Similarity 32.0%; Pred. No. 9;
Matches 24; Conservative 16; Mismatches 25; Indels 10; Gaps 4;
Molecules type: DNA

Qy 41 MKKLSDLAEAWAPSPRLQAOQLPAPVCHHPAL--PDLQPVCAQOEASSIFKTLRTIAN 98
Db 361 MRELIEASLERNPVHRPAADLL-----KHEALNPREDQPCQSLD-SALLERKLLSRK 415

Qy 99 DCELCVNVA---CTG 110
Db 416 ELELPENIADSSCTG 430

RESULT 14
S63453
probable RNA helicase SUV3, ATP-dependent, precursor - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein LPB2w; protein YPL029w
C:Species: Saccharomyces cerevisiae
C:Date: 16-May-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C:Accession: S63453; A46190; S27462
R:Wang, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Frieseen, J.D.; Hall, J.; Storme, R.K.; Vo
submitted to the EMBL Data Library, September 1995
A:Reference number: S63452
A:Accession: S63453
A:Molecule type: DNA
A:Residues: 1-737 <WAN>
A:Cross-references: UNIPROT:P32580; EMBL:U36624; NID:g1276642; PIDN:AAB68158.1; PID:g101
R:Stepien, P.P.; Margossian, S.P.; Landman, D.; Butow, R.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 6813-6817, 1992
A:Title: The yeast nuclear gene suv3 affecting mitochondrial post-transcriptional proces
A:Reference number: A46190; MUID:92357722; PMID:1379722
A:Accession: A46190
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-164, 'R', '166-597', 'DL', '600-615', 'A', '617-636', 'D', '638-663', 'D', '665-737' <STE>
A:Cross-references: EMBL:M91167
A:Note: sequence extracted from NCBI backbone (NCBI:P:111103)
R:Stepien, P.P.; Margossian, S.P.; Landman, D.; Butow, R.A.
submitted to the EMBL Data Library, April 1992
A:Description: The yeast nuclear gene suv3 affecting mitochondrial post-transcriptional
A:Reference number: S27462
A:Accession: S27462
A:Molecule type: DNA
A:Residues: 1-164, 'R', '166-663', 'D', '665-737' <ST2>
A:Cross-references: EMBL:M91167; NID:g172797; PIDN:AAA35135.1; PID:g172798
C:Genetics:
A:Gene: SGD:SUV3
A:Cross-references: SGD:S0005950; MIPS:YPL029w
A:Map position: 16L
A:Genome: nuclear
C:Function:
A:Description: Involved in mitochondrial translation and pre-mRNA splicing
C:Keywords: ATP; mitochondrion; nucleotide binding; P-loop
F:1-25/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:26-737/Product: probable RNA helicase #status predicted <MAT>
F:239-246/Region: nucleotide-binding motif A (P-loop)
F:320-325/Region: nucleotide-binding motif B
F:324-327/Region: DEAD/H motif #status atypical

Query Match 12.3%; Score 71; DB 2; Length 737;
Best Local Similarity 26.6%; Pred. No. 19;
Matches 21; Conservative 14; Mismatches 18; Indels 26; Gaps 3;
Molecules type: DNA

Qy 24 TQSVYIQYQGFVRVQLSESM-----KKLSDLAEAWAP-----SPRLQAO 59
Db 72 SNNVYLQDSSFKQNLCKAMQFIYNDKLSLSDAKQVPIKNLAWLKLRDYIYQQLKDKPLQAO 131

Qy 60 QSLLPVCH--HPALPQDL 76

Search completed: March 26, 2005, 16:49:40
Job time : 23.708 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:51:20 ; Search time 71.0357 Seconds
(without alignments)
129.758 Million cell updates/sec

Title: US-10-775-481A-3

Perfect score: 18

Sequence: 1 NTFYCCCLCCYPACAGCN 18

Scoring table: Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	1 HSTB_ECOLI	P01560 escherichia
2	10	55.6	18	2 Q7M0U3	Q7m0u3 citrobacter
3	10	55.6	61	2 Q6VEG9	Q6veg9 escherichia
4	10	55.6	72	1 HST1_ECOLI	P01559 escherichia
5	7	38.9	61	2 Q6VEG7	Q6veg7 escherichia
6	7	38.9	61	2 Q6VEG8	Q6veg8 escherichia
7	7	38.9	72	1 HST2_ECOLI	Q47185 escherichia
8	7	38.9	72	1 HST3_ECOLI	P07965 escherichia
9	7	38.9	120	2 Q858Z4	Q858z4 bacterioph
10	6	33.3	66	1 HST_YERKR	P31518 yersinia kr
11	6	33.3	71	1 HST_YEREN	P74977 yersinia en
12	6	33.3	71	1 HSTB_YEREN	O50319 yersinia en
13	6	33.3	72	1 HSTC_YEREN	Q8x4m8 escherichia
14	6	33.3	90	2 Q8X4M8	Q7v2z2 stx1 conver
15	6	33.3	96	2 Q7Y2Z2	Q9t1l3 bacterioph
16	6	33.3	96	2 Q9T1L3	Q8pnn9 xanthomonas
17	6	33.3	130	2 Q8PNN9	Q8cbh7 mus musculu
18	6	33.3	252	2 Q8CBH7	P54145 caenorhabdi
19	6	33.3	534	1 AMT1_CABEL	Q8vui3 desulfovibr
20	6	33.3	556	2 Q8VUI3	Q8vuf2 mus musculu
21	6	33.3	607	2 Q8VUF2	Q7tmr1 mus musculu
22	6	33.3	609	2 Q7TMR1	Q8c6v9 mus musculu
23	6	33.3	738	2 Q8C6V9	Q8k0j1 mus musculu
24	6	33.3	876	2 Q8K0J1	Q9lht5 arabidopsis
25	6	33.3	1030	2 Q9LHT5	Q8cjm2 streptomyce
26	6	33.3	1210	2 Q8CJM2	Q8c2f9 mus musculu
27	6	33.3	1282	2 Q8C2F9	Q071l3 mus musculu
28	6	33.3	2483	1 MPRI_MOUSE	P55936 didelphis m
29	5	27.8	15	1 GUAN_DIDMA	Q86rb2 conus geogr
30	5	27.8	40	1 CXAC_CONGE	Q83ak0 coxiella bu
31	5	27.8	45	2 Q83AK0	

RESULT 1

ID	HSTB_ECOLI	STANDARD;	PRT;	18 AA.
AC	P01560;			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	05-JUL-2004	(Rel. 44, Last annotation update)		
DE	Heat-stable enterotoxin ST-2 (ST-B).			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN=O42:K86:H37 / 18D / ETEC;			
RX	MEDLINE=81264141; PubMed=7021541;			
RA	Chan S.-K., Giannella R.A.;			
RT	"Amino acid sequence of heat-stable enterotoxin produced by			
RT	Escherichia coli pathogenic for man.";			
RL	J. Biol. Chem. 256:7744-7746(1981).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5;			
RA	Shimomishi Y., Hidaka Y., Koizumi M., Hane M.,imoto S., Takeda T.,			
RA	Miwatani T., Takeda Y.;			
RT	"Mode of disulfide bond formation of a heat-stable enterotoxin (STH)			
RT	produced by a human strain of enterotoxigenic Escherichia coli.";			
RL	FESS Lett. 215:165-170(1987).			
CC	-1- FUNCTION: Toxin which activates the particulate form of guanylate			
CC	cyclase and increases cyclic GMP levels within the host intestinal			
CC	epithelial cells.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: Belongs to the heat-stable enterotoxin family.			
DR	PIR; A01823; Q8EC2.			
DR	HSRP; P01559; IETN.			
DR	InterPro; IPR001489; Enterotoxin HS.			
DR	Pfam; PF02048; Enterotoxin HS; 1.			
DR	PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.			
KW	Direct protein sequencing; Enterotoxin; Toxin.			
FT	DISULFID 5 10			
FT	DISULFID 6 14			
FT	DISULFID 9 17			
SQ	SEQUENCE 18 AA; 1978 MW; DDC975F49D600650 CRC64;			

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NTFYCCCLCCYPACAGCN 18

Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 2


```
Q7MOU3
ID Q7MOU3 PRELIMINARY; PRT; 18 AA.
AC Q7MOU3
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat-stable enterotoxin ST-1a.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE.
RA MEDLINE=89108617; PubMed=2912902;
RA Guarino A., Giannella R., Thompson M.R.;
RT "Citrobacter freundii produces an 18-amino-acid heat-stable
RT enterotoxin identical to the 18-amino-acid Escherichia coli heat-
RT stable enterotoxin (ST 1a).";
RL Infect. Immun. 57:649-652(1989).
DR PIR; A60103; A60103.
DR HSP; P01559; IETN.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
SQ SEQUENCE 18 AA; 1978 MW; D4D975F49D60064F CRC64;

Query Match 55.6%; Score 10; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCC 10
Db 1 NTFYCCCLCC 10

RESULT 3
Q6VEG9 PRELIMINARY; PRT; 61 AA.
ID Q6VEG9
AC Q6VEG9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat-stable enterotoxin ST-1a (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Reischl U., Youssef M.T., Wolf H., Hyttia-Trees E., Strockbine N.A.;
RT "Real-time fluorescence PCR assays for detection and characterization
RT of heat-labile I and heat-stable I enterotoxin genes from
RT enterotoxigenic Escherichia coli.";
RL ENBL; AY342057; AAQ92974.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
FT NON_TER 1
SQ SEQUENCE 61 AA; 6927 MW; 646D4AE2F8999957 CRC64;

Query Match 55.6%; Score 10; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCC 10
Db 44 NTFYCCCLCC 53
```

```
RESULT 4
HSTL_ECOLI STANDARD; PRT; 72 AA.
ID HSTL_ECOLI
AC P01559; Q47653;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Heat-stable enterotoxin ST-1a/ST-P precursor.
GN Name=stai;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=Tn1681;
RX MEDLINE=81054703; PubMed=6254008;
RA So M., McCarthy B.J.;
RT "Nucleotide sequence of the bacterial transposon Tn1681 encoding a
RT heat-stable (ST) toxin and its identification in enterotoxigenic
RT Escherichia coli strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4011-4015(1980).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O42:K86:H37 / 18D / ETEC;
RX MEDLINE=90368614; PubMed=2203756;
RA Dallas W.S.;
RT "The heat-stable toxin I gene from Escherichia coli 18D.";
RL J. Bacteriol. 172:5490-5493(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=85249571; PubMed=2990268;
RA Sekizaki T., Akashi H., Terakado N.;
RT "Nucleotide sequences of the genes for Escherichia coli heat-stable
RT enterotoxin I of bovine, avian, and porcine origins.";
RL Am. J. Vet. Res. 46:909-912(1985).
RN [4]
RP DISULFIDE BONDS.
RX MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5;
RA Shimonishi Y., Hidak Y., Koizumi M., Hane M., Aimoto S., Takeda T.,
RA Miwatani T., Takeda Y.;
RT "Mode of disulfide bond formation of a heat-stable enterotoxin (STh)
RT produced by a human strain of enterotoxigenic Escherichia coli.";
RL FEBS Lett. 215:165-170(1987).
RN [5]
RP PROCESSING.
RX MEDLINE=90368584; PubMed=2203746;
RA Okamoto K., Takahara M.;
RT "Synthesis of Escherichia coli heat-stable enterotoxin STp as a pre-
RT pro form and role of the pro sequence in secretion.";
RL J. Bacteriol. 172:5260-5265(1990).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (0.89 ANGSTROMS) OF 59-71.
RX MEDLINE=94312375; PubMed=8038153;
RA Sato T., Ozaki H., Hata Y., Kitagawa Y., Kataube Y., Shimonishi Y.;
RT "Structural characteristics for biological activity of heat-stable
RT enterotoxin produced by enterotoxigenic Escherichia coli: X-ray
RT crystallography of weakly toxic and nontoxic analogs.";
RL Biochemistry 33:8641-8650(1994).
CC -1- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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```


or send an email to license@isb-sib.ch).

```
CC -----
CC EMBL; V00612; CAA23883.1; -.
DR EMBL; M58746; AAA62776.1; -.
DR EMBL; M25607; AAA24653.1; -.
DR PIR; A01822; QHEC1.
DR PDB; 1ETL; X-ray; @=59-71.
DR PDB; 1ETM; X-ray; @=-.
DR PDB; 1ETN; X-ray; @=-.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW 3D-structure; Enterotoxin; Signal; Toxin; Transposable element.
FT SIGNAL 1 19
FT PROPEP 20 54
FT PEPTIDE 55 72 Heat-stable enterotoxin ST-1A/ST-P.
FT DISULFID 59 64
FT DISULFID 60 68
FT DISULFID 63 71
FT CONFLICT 70 70 G -> P (in Ref. 3).
FT TURN 61 62
FT TURN 66 67
FT TURN 69 70
SQ SEQUENCE 72 AA; 8075 MW; 92E8B766B3988264 CRC64;
```

Query Match 55.6%; Score 10; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCC 10
Db 55 NTFYCCCLCC 64
|||||

RESULT 5

```
Q6VEG7 ID Q6VEG7 PRELIMINARY; PRT; 61 AA.
AC Q6VEG7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Heat-stable enterotoxin ST Ib (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R544;
RX PubMed=15364995;
RA Reischl U., Yousef M.T., Wolf H., Hyytia-Trees E., Strockbine N.A.;
RT "Real-time fluorescence PCR assays for detection and characterization
of heat-labile I and heat-stable I enterotoxin genes from
enterotoxigenic Escherichia coli.";
RL J. Clin. Microbiol. 42:4092-4100(2004).
DR EMBL; AY342059; AAQ92976.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
FT NON TER 1 1
SQ SEQUENCE 61 AA; 6556 MW; 89788D3FAB3DCA0A CRC64;
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Query Match 38.9%; Score 7; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCCCLCC 10
Db 47 YCCCLCC 53
|||||

RESULT 6

```
Q6VEG8 ID Q6VEG8 PRELIMINARY; PRT; 61 AA.
AC Q6VEG8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Heat-stable enterotoxin ST Ib (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C4046;
RX PubMed=15364995;
RA Reischl U., Yousef M.T., Wolf H., Hyytia-Trees E., Strockbine N.A.;
RT "Real-time fluorescence PCR assays for detection and characterization
of heat-labile I and heat-stable I enterotoxin genes from
enterotoxigenic Escherichia coli.";
RL J. Clin. Microbiol. 42:4092-4100(2004).
DR EMBL; AY342058; AAQ92975.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
FT NON TER 1 1
SQ SEQUENCE 61 AA; 6658 MW; 1D75955D7AF0DED2 CRC64;
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Query Match 38.9%; Score 7; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YCCCLCC 10
Db 47 YCCCLCC 53
|||||

RESULT 7

```
HST2_ECOLI ID HST2_ECOLI STANDARD; PRT; 72 AA.
AC Q47185;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin A2 precursor (STA2).
GN Name=sta2;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=2643580;
RA Guzman-Verduzio L.M., Kupersztich Y.M.;
RT "Rectification of two Escherichia coli heat-stable enterotoxin allele
sequences and lack of biological effect of changing the carboxy-
terminal tyrosine to histidine.";
RL Infect. Immun. 57:645-648(1989).
CC -1- FUNCTION: Toxin which activates the particulate form of guanylate
cyclase and increases cyclic GMP levels within the host intestinal
epithelial cells.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.
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CC -----AAA23729.1; --
DR EMBL; M18345; AAA23729.1; --
DR PIR; JS0292; QHECIB.
DR HSP; P01559; IETN.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW Enterotoxin; Signal; Toxin.
FT SIGNAL 1 19 Potential.
FT PROPEP 20 53 By similarity.
FT PEPTIDE 54 72 Heat-stable enterotoxin A2.
FT DISULFID 59 64 By similarity.
FT DISULFID 60 68 By similarity.
FT DISULFID 63 71 By similarity.
FT DISULFID 63 71 By similarity.
SQ SEQUENCE 72 AA; 7895 MW; D8785030605260 CRC64;

Query Match 38.9%; Score 7; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCCCLCC 10
Db 58 YCCCLCC 64

RESULT 8
HST3_ECOLI STANDARD; PRT; 72 AA.
ID HST3_ECOLI
AC P07965; P26588;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin A3/A4 precursor (ST3/ST4) (ST-IB) (ST-H).
GN Name:st3; Synonym:st3a4;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
SQ SEQUENCE FROM N.A.
RP MEDLINE=89202548; PubMed=3071819;
RX Stieglitz H., Cervantes L., Robledo R., Fonseca R., Covarrubias L.,
RA Bolivar F., Kupersztosch Y.M.;
RT "Cloning, sequencing, and expression in Ficol1-generated minicells of
RT an Escherichia coli heat-stable enterotoxin gene.";
RL Plasmid 20:42-53 (1988).
RN [2]
SQ SEQUENCE FROM N.A.
RP STRAIN=153837-2;
RX MEDLINE=83184648; PubMed=6341230;
RA Moseley S.L., Hardy J.W., Huq M.I., Echeverria P., Falkow S.;
RT "Isolation and nucleotide sequence determination of a gene encoding a
RT heat-stable enterotoxin of Escherichia coli.";
RL Infect. Immun. 39:1167-1174 (1983).
RN [3]
SQ SEQUENCE FROM N.A.
RP MEDLINE=90273381; PubMed=2190361; DOI=10.1016/0041-0101(90)90085-L;
RX Zhou X., Shen L.P., Chi C.W.;
RA "Isolation and nucleotide sequence determination of a gene encoding a
RT heat-stable enterotoxin of Escherichia coli.";
RL Toxicon 28:453-456 (1990).
RN [4]
SQ SEQUENCE FROM N.A.
RP MEDLINE=89108616; PubMed=2643580;
RX Guzman-Verduzco L.M., Kupersztosch Y.M.;
RA "Rectification of two Escherichia coli heat-stable enterotoxin allele
RT sequences and lack of biological effect of changing the carboxy-
RT terminal tyrosine to histidine.";
RL Infect. Immun. 57:645-648 (1989).
RN [5]
SQ SEQUENCE FROM N.A.
RP MEDLINE=90034194; PubMed=2680769; DOI=10.1016/0378-1119(89)90182-0;
RX Dwarakanath P., Visweswariah S.S., Subrahmanyam Y.V.B.K., Shanthi G.,

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RA Jagannatha H.M., Balganesht S.;
RT "Cloning and hyperexpression of a gene encoding the heat-stable toxin
RT of Escherichia coli.";
RL Gene 81:219-226 (1989).
RN [6]
SQ SEQUENCE OF 54-72.
RX MEDLINE=83105138; PubMed=6759126;
RA Aimoto S., Takao T., Shimonishi Y., Hara S., Takeda T., Takeda Y.,
RA Miwatani T.;
RT "Amino-acid sequence of a heat-stable enterotoxin produced by human
RT enterotoxigenic Escherichia coli.";
RL Eur. J. Biochem. 129:257-263 (1982).
RN [7]
SQ SEQUENCE OF 54-72.
RX MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5;
RA Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T.,
RA Miwatani T., Takeda Y.;
RT "Mode of disulfide bond formation of a heat-stable enterotoxin (Sth)
RT produced by a human strain of enterotoxigenic Escherichia coli.";
RL FEBS Lett. 215:165-170 (1987).
RN [8]
SQ SEQUENCE OF 54-72.
RX MEDLINE=90251166; PubMed=2187146;
RA Rasheed J.K., Guzman-Verduzco L.M., Kupersztosch Y.M.;
RT "Two precursors of the heat-stable enterotoxin of Escherichia coli:
RT evidence of extracellular processing.";
RL Mol. Microbiol. 4:265-273 (1990).
CC -1- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.
CC -----
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CC -----
CC EMBL; J03311; AAA24652.1; --
CC EMBL; M34916; AAA23990.1; --
CC EMBL; M18346; AAA23730.1; --
CC EMBL; M29255; AAA24686.1; --
CC PIR; JS0292; QHECIB.
CC PIR; JT0373; QHEC4.
CC HSP; P01559; IETN.
CC InterPro; IPR001489; Enterotoxin HS.
CC Pfam; PF02048; Enterotoxin HS; 1.
CC PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW Direct protein sequencing; Enterotoxin; Signal; Toxin.
FT SIGNAL 1 19
FT PROPEP 20 53 Heat-stable enterotoxin A3/A4.
FT PEPTIDE 54 72
FT DISULFID 59 64
FT DISULFID 60 68
FT DISULFID 63 71
FT CONFLICT 19 19 A -> P (in Ref. 2).
SQ SEQUENCE 72 AA; 7909 MW; 1C5C9292BFCA6BA CRC64;

Query Match 38.9%; Score 7; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YCCCLCC 10
Db 58 YCCCLCC 64

RESULT 9
Q85824 PRELIMINARY; PRT; 120 AA.
ID Q85824

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Q85824;
 AC 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Gp7.
 OS Bacteriophage phi-BT1.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC Lambda-like viruses.
 ON NCBI_TaxID=225588;
 RX MEDLINE=22803275; PubMed=12923110;
 RX DOI=10.1128/JB.185.17.5320-5323.2003;
 RA Gregory M.A., Till R., Smith M.C.M.;
 RT "Integration Site for Streptomyces Phage {phi}BT1 and Development of
 RT Site-Specific Integrating Vectors.";
 RL J. Bacteriol. 185:5320-5323(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Gregory M.A.;
 RT "Characterisation and Evolution of Homoimmune Streptomyces
 RT Bacteriophages";
 RL Thesis (2000). Department of Genetics, University of Nottingham,
 RL Nottingham, UNITED KINGDOM.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Smith M.C.M.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ550940; CAD80131.1; -;
 DR GO; GO:0004519; F:endonuclease activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR002711; HNH.
 DR InterPro; IPR003615; HNH_nuc.
 DR Pfam; PF01844; HNH; 1.
 DR SMART; SM00507; HNHc; 1.
 SQ SEQUENCE 120 AA; 13827 MW; 2EAC16389699723 CRC64;
 Query Match 38.9%; Score 7; DB 2; Length 120;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 12 PACACGN 18
 Db 94 PACACGN 100
 |||||
 RESULT 10
 ID HST_YERKR STANDARD; PRT; 66 AA.
 AC P31518;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat-stable enterotoxin precursor.
 GN Name=yet;
 OS Yersinia kristensenii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=28152;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IP490 / Serotype O:12,25;
 RA Ibrahim A., Liesack W., Stackebrandt E.;
 RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Toxin which activates the particulate form of guanylate
 CC cyclase and increases cyclic GMP levels within the host intestinal
 CC epithelial cells (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.
 CC
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 CC -----
 DR EMBL; X69218; CAA49152.1; -;
 DR PIR; S31652; S31652.
 DR HSSP; P01559; IETN.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1.
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 KW Enterotoxin; Signal.
 FT SIGNAL 1 19 Potential.
 FT PROPEP 20 50
 FT CHAIN 51 66 Heat-stable enterotoxin (By similarity).
 FT DISULFID 54 59 By similarity.
 FT DISULFID 55 63 By similarity.
 FT DISULFID 58 66 By similarity.
 SQ SEQUENCE 66 AA; 7068 MW; 27BE7006675CC075 CRC64;
 Query Match 33.3%; Score 6; DB 1; Length 66;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 12 PACACG 17
 Db 61 PACACG 66
 |||||
 RESULT 11
 ID HSTA_YEREN STANDARD; PRT; 71 AA.
 AC P07593;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat-stable enterotoxin A precursor (YST-A).
 GN Name=yetA; Synonym=yet;
 OS Yersinia enterocolitica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=630;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Serotype O:8;
 RX MEDLINE=93051243; PubMed=1427005; DOI=10.1016/0378-1097(92)90364-T;
 RA Ibrahim A., Liesack W., Pike S., Stackebrandt E.;
 RT "The polymerase chain reaction: an epidemiological tool to
 RT differentiate between two clusters of pathogenic Yersinia
 RT enterocolitica strains.";
 RL FEMS Microbiol. Lett. 76:63-66(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W1024 / Serotype O:9;
 RX MEDLINE=90354067; PubMed=2201642;
 RA Delor I., Kaeckenbeeck A., Wauters G., Cornelis G.R.;
 RT "Nucleotide sequence of yet, the Yersinia enterocolitica gene encoding
 RT the heat-stable enterotoxin, and prevalence of the gene among
 RT pathogenic and nonpathogenic yersiniae.";
 RL Infect. Immun. 58:2983-2988(1990).
 RN [3]
 RP SEQUENCE OF 54-71.
 RC MEDLINE=86004705; PubMed=4043080;
 RA Takao T., Tomimaga N., Yoshimura S., Shimonishi Y., Hara S., Inoue T.,
 RA Miyama A.;
 RT "Isolation, primary structure and synthesis of heat-stable enterotoxin
 RT produced by Yersinia enterocolitica.";
 RL Eur. J. Biochem. 152:199-206(1985).
 CC -1- FUNCTION: Toxin which activates the particulate form of guanylate
 CC cyclase and increases cyclic GMP levels within the host intestinal
 CC epithelial cells.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- INDUCTION: In cultured cells, expressed only at temperatures <30

degrees Celsius. Under conditions of high osmolarity and alkaline pH (as it is the case in the host's intestine), it is expressed at 37 degrees Celsius.

-1- SIMILARITY: Belongs to the heat-stable enterotoxin family.

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EMBL; X65999; CA446801.1; -;
EMBL; U02335; AAI18472.1; -;
PIR; S25659; S25659.
HSSP; P01559; IETN.
InterPro; IPR001489; Enterotoxin HS.
Pfam; PF02048; Enterotoxin HS; 1.
PROSITE; PS00273; ENTEROTOXIN_H STABLE; 1.
Direct protein sequencing; Enterotoxin; Signal; Toxin.
SIGNAL 1 19 Potential.
FT PROPEP 20 53 Heat-stable enterotoxin A.
FT CHAIN 54 71 By similarity.
FT DISULFID 59 64 By similarity.
FT DISULFID 60 68 By similarity.
FT DISULFID 63 71 By similarity.
FT VARIANT 48 48 L->S.
SQ SEQUENCE 71 AA; 7494 MW; 022F99B3800C861B CRC64;

Query Match 33.3%; Score 6; DB 1; Length 71;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 PACAGC 17
Db 66 PACAGC 71

RESULT 12
HSTB_YEREN STANDARD; PRT; 71 AA.
AC P74977;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin B precursor (Y-STB).
GN Names:yStB;
OS Yersinia enterocolitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=84-50 / Serotype O:5;
RX MEDLINE=98008784; PubMed=9344780; DOI=10.1006/mpat.1997.0146;
RA Ramamurthy T., Yoshino K., Huang X., Nair G.B., Carniel E.,
RA Maruyama T., Fukushima H., Takeda T.;
RT "The novel heat-stable enterotoxin subtype gene (yStB) of Yersinia enterocolitica: nucleotide sequence and distribution of the yst genes.";
RT Microb. Pathog. 23:189-200(1997).
RN [2]
RP SEQUENCE OF 20-72.
RC STRAIN=Serotype O:3;
RX MEDLINE=95246844; PubMed=7729521; DOI=10.1016/0014-5793(95)00267-D;
RA Yoshino K., Takao T., Huang X., Murata H., Nakao H., Takeda T.,
RA Shimomishi Y.;
RT "Characterization of a highly toxic, large molecular size heat-stable enterotoxin produced by a clinical isolate of Yersinia enterocolitica.";
RT FEBS Lett. 362:319-322(1995).
CC -1- FUNCTION: Toxin which activates the particulate form of guanylate cyclase and increases cyclic GMP levels within the host intestinal epithelial cells. Could play an important role in pathogenesis.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.
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EMBL; D88145; BAA13544.1; -;
HSSP; P01559; IETN.
InterPro; IPR001489; Enterotoxin HS.
Pfam; PF02048; Enterotoxin HS; 1.
PROSITE; PS00273; ENTEROTOXIN_H STABLE; 1.
Direct protein sequencing; Enterotoxin; Signal; Toxin.
SIGNAL 1 19 Potential.
FT PROPEP 20 52 Heat-stable enterotoxin B.
FT CHAIN 53 71 By similarity.
FT DISULFID 59 64 By similarity.
FT DISULFID 60 68 By similarity.
FT DISULFID 63 71 By similarity.
SQ SEQUENCE 71 AA; 7670 MW; ED6E9F61ACDD4F50 CRC64;

Query Match 33.3%; Score 6; DB 1; Length 71;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 PACAGC 17
Db 66 PACAGC 71

RESULT 13
HSTC_YEREN STANDARD; PRT; 72 AA.
AC O50319;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin C precursor (Y-STC).
GN Name:yStC;
OS Yersinia enterocolitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=86-11;
RX MEDLINE=97202479; PubMed=9049998; DOI=10.1006/mpat.1996.0094;
RA Huang X., Yoshino K., Nakao H., Takeda T.;
RT "Nucleotide sequence of a gene encoding the novel Yersinia enterocolitica heat-stable enterotoxin that includes a pro-region-like sequence in its mature toxin molecule.";
RT Microb. Pathog. 22:89-97(1997).
RN [2]
RP SEQUENCE OF 20-72.
RC STRAIN=Serotype O:3;
RX MEDLINE=95246844; PubMed=7729521; DOI=10.1016/0014-5793(95)00267-D;
RA Yoshino K., Takao T., Huang X., Murata H., Nakao H., Takeda T.,
RA Shimomishi Y.;
RT "Characterization of a highly toxic, large molecular size heat-stable enterotoxin produced by a clinical isolate of Yersinia enterocolitica.";
RT FEBS Lett. 362:319-322(1995).
CC -1- FUNCTION: Toxin which activates the particulate form of guanylate cyclase and increases cyclic GMP levels within the host intestinal epithelial cells. Highly toxic.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.
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DR HSP; P01559; IETN.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1.
 DR PROSITE; PS00273; ENTEROTOXIN_H STABLE; 1.
 KW Direct protein sequencing; Enterotoxin; Signal; Toxin.
 FT SIGNAL 1 19
 FT CHAIN 20 72 Heat-stable enterotoxin C.
 FT DISULFID 60 65 By similarity.
 FT DISULFID 61 69 By similarity.
 FT DISULFID 64 72 By similarity.
 SQ SEQUENCE 72 AA; 7639 MW; 7C0D83893C2F981D CRC64;

Query Match 33.3%; Score 6; DB 1; Length 72;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCELC 10
 Db 60 CCELC 65

RESULT 14

Q8X4M8 PRELIMINARY; PRT; 90 AA.
 AC Q8X4M8;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Putative lysis protein S of prophage CP-933V.
 GN OrderedLocusNames=z3340;
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
 RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
 RL Nature 408:529-533(2001).
 DR EMBL; AB005442; AAG57224.1; -.
 DR PIR; D85845; D85845.
 DR Pfam; PF04971; Lysis_S; 1.
 KW Complete proteome.
 SQ SEQUENCE 90 AA; 10060 MW; 680A0C48B94B2AF CRC64;

Query Match 33.3%; Score 6; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FYCCEL 8
 Db 7 FYCCEL 12

RESULT 15

Q7Y222 PRELIMINARY; PRT; 96 AA.
 AC Q7Y222;
 DT 01-OCT-2003 (TReMBLrel. 25, Created)
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Lysis protein.
 OS Stx1 converting bacteriophage.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC Lambda-like viruses.
 OX NCBI_TaxID=194948;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Stx1 phage;
 RX MEDLINE=22697399; PubMed=12813092;
 RX DOI=10.1128/JB.185.13.3966-3971.2003;
 RA Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T.,
 RA Takeda Y., Yamasaki S.;
 RT "Genome analysis of a novel Shiga toxin 1 (Stx1)-converting phage
 RT which is closely related to Stx2-converting phages but not to other
 RT Stx1-converting phages";
 RL J. Bacteriol. 185:3966-3971(2003).
 DR EMBL; AP005153; BAC77969.1; -.
 DR InterPro; IPR007054; Lysis_S;
 DR Pfam; PF04971; Lysis_S; 1.
 SQ SEQUENCE 96 AA; 10684 MW; CFI562C30DA56B19 CRC64;

Query Match 33.3%; Score 6; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FYCCEL 8
 Db 13 FYCCEL 18

Search completed: March 26, 2005, 17:24:51
 Job time : 72.0357 secs

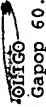
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:49:45 ; Search time 84.4821 Seconds
(without alignments)
86.982 Million cell updates/sec

Title: US-10-775-481A-5
Perfect score: 19
Sequence: 1 NSSNYCCELCNPCNGCY 19

Scoring table: 
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	2	AAR85948
2	19	100.0	19	2	AY40510 ST rec
3	19	100.0	19	8	ADR45825 Amino aci
4	15	78.9	18	2	AAR85970 ST Ib rec
5	15	78.9	18	2	AY40532 ST recept
6	15	78.9	18	8	ADR45846 Amino aci
7	15	78.9	19	2	AAR95923 Enterotox
8	15	78.9	19	2	AY02386 Heat stab
9	15	78.9	19	2	AY29608 Escherich
10	15	78.9	19	2	AY06972 E. coli h
11	15	78.9	19	2	AY02398 Heat stab
12	15	78.9	19	4	AAM51879 Human the
13	15	78.9	19	6	AAO16204 E coli sm
14	15	78.9	19	6	ABG74825 E. coli h
15	15	78.9	19	7	ADC14120 Heat stab
16	15	78.9	19	7	ADC14123 Modified
17	15	78.9	19	7	ADC14121 Modified
18	15	78.9	19	8	ADR48340 Bacterial
19	15	78.9	19	8	ADR48360 Analgesic
20	15	78.9	19	8	ADR48359 Analgesic
21	15	78.9	19	8	ADR48398 Peptide u
22	15	78.9	19	8	ADR48329 E. coli S
23	15	78.9	19	8	ADR48404 GC-C acti
24	15	78.9	21	8	ADR48372 Analgesic
25	15	78.9	21	8	ADR48413 GC-C acti

26	15	78.9	21	8	ADR48373	Adr48373 Analgesic
27	15	78.9	21	8	ADR48414	Adr48414 GC-C acti
28	15	78.9	72	2	AAR20352	Aar20352 Sequence
29	15	78.9	72	2	AAR71975	Aar71975 E. coli s
30	15	78.9	72	8	ADR48356	Adr48356 Immature
31	14	73.7	17	2	AAR85971	Aar85971 ST Ib rec
32	14	73.7	17	2	AY40533	AY40533 ST recept
33	14	73.7	17	8	ADR45847	Adr45847 Amino aci
34	14	73.7	18	2	AAR85976	Aar85976 ST Ib rec
35	14	73.7	18	2	AY40538	AY40538 ST recept
36	14	73.7	18	8	ADR45852	Adr45852 Amino aci
37	14	73.7	19	4	AAB83216	Aab83216 Escherich
38	13	68.4	16	2	AAR85972	Aar85972 ST Ib rec
39	13	68.4	16	2	AY40534	AY40534 ST recept
40	13	68.4	16	8	ADR45848	Adr45848 Amino aci
41	13	68.4	17	2	AAR85977	Aar85977 ST Ib rec
42	13	68.4	17	2	AY40539	AY40539 ST recept
43	13	68.4	17	8	ADR45853	Adr45853 Amino aci
44	12	63.2	15	2	AAR85973	Aar85973 ST Ib rec
45	12	63.2	15	2	AY40535	AY40535 ST recept

ALIGNMENTS

RESULT 1

AAR85948
ID AAR85948 standard; peptide; 19 AA.
XX
AC AAR85948;
XX
DT 19-JAN-1996 (first entry)
DE ST Ib receptor ligand portion.
XX
KW ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
KW colorectal; metastasis.
XX
OS Escherichia coli.
XX
PN WO9511694-A1.
XX
PD 04-MAY-1995.
XX
PF 26-OCT-1994; 94WO-US012232.
XX
PR 26-OCT-1993; 93US-00141892.
PR 13-SEP-1994; 94US-00105056.
XX
(UYJE-) UNIV JEFFERSON THOMAS.
XX
Waldman SA;
XX
WPI; 1995-178646/23.
XX
Conjugated cpds. which specifically bind to colorectal cancer cells -
comprise heat-stable toxin receptor binding moiety and active moiety
which may be a therapeutic agent or a radioactive agent.
XX
Claim 3; Page 116; 133pp; English.
XX
New conjugated compounds are provided which consist of (1) an ST receptor
binding moiety and (2) an active moiety which is a radio- stable agent.
XX
CC 'ST' refers to a heat stable toxin produced by E.coli and other
CC organisms. Especially the radiostable agent is a therapeutic agent (e.g.
CC methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive
CC isotope) or nucleic acid; and the compound is used for the detection,
CC imaging or treatment of colorectal tumours, particularly metastasised
CC tumours. The present sequence is a specific example of an ST receptor
CC binding peptide which can be used in the conjugate
XX
SQ Sequence 19 AA;

```
Query Match      100.0%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPACNGCY 19
Db 1 NSSNYCCCLCCNPACNGCY 19

RESULT 2
AAY40510
ID AAY40510 standard; peptide; 19 AA.
XX AC AAY40510;
XX DT 03-DEC-1999 (first entry)
XX DE ST receptor peptide ST 1b.
XX KW Conjugated compound; ST receptor; heat-stable; toxin; colorectal cancer.
XX OS Escherichia coli.
XX PN US5962220-A.
XX PD 05-OCT-1999.
XX PF 06-JUN-1995; 95US-00467920.
XX PR 26-OCT-1993; 93US-00141892.
XX PA (UYJE-) UNIV JEFFERSON THOMAS.
XX PI Waldman SA;
XX DR WPI; 1999-571264/48.
XX DT N-PSDB; AAZ07541.
XX PT Conjugated compound comprising a receptor moiety and active moiety,
XX PT useful for the treatment/prevention of colorectal cancer.
XX PS Claim 1; Col 21-22; 23pp; English.
XX CC The invention relates to a conjugated compound that comprises a ST (heat-
XX CC stable toxin) receptor moiety selected from one of the sequences shown in
XX CC AAY40508-Y40559 and an active moiety (antitense molecule). The compound
XX CC is useful for the treatment of colorectal cancer. The use of the
XX CC conjugated compound is advantageous compared to antibodies since it binds
XX CC specifically to colorectal cells and has no toxic effect on normal cells.
XX CC The present sequence represents the amino acid sequence of a ST receptor
XX CC peptide ST 1b
XX SQ Sequence 19 AA;

Query Match      100.0%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPACNGCY 19
Db 1 NSSNYCCCLCCNPACNGCY 19

RESULT 3
ADR45825
ID ADR45825 standard; peptide; 19 AA.
XX AC ADR45825;
XX DT 18-NOV-2004 (first entry)
XX DE Amino acid sequence of heat stable toxin ST 1b.
XX PD 04-MAY-1995.
XX XX

KW heat stable toxin; ST; ST receptor; colorectal cancer; gastric cancer;
KW oesophageal cancer; colorectal cell; gastric cell; oesophageal cell;
KW ST 1b.
XX Unidentified.
XX OS WO2004071436-A2.
XX PN 26-AUG-2004.
XX PD 10-FEB-2004; 2004WO-US003765.
XX PF 10-FEB-2003; 2003US-0446730P.
XX PR (UYJE-) UNIV JEFFERSON THOMAS.
XX PA Waldman SA, Pitari GM, Park J, Schulz S, Wolfe HR;
XX PI WPI; 2004-615913/59.
XX DR N-PSDB; ADR45824.
XX XX
XX Increasing ST receptor molecules on the surface of a colorectal, gastric
XX PT or esophageal cancer cell to treat these cancers comprises administering
XX PT ST receptor ligand molecules that bind to ST receptors on the surface of
XX PT the cancer cell.
XX PS Claim 6; SEQ ID NO 5; 97pp; English.
XX CC The specification describes a method for increasing the number of heat
XX CC stable toxin (ST) receptor molecules on the surface of a metastasised
XX CC colorectal cancer cell. The method comprises administering, by continuous
XX CC infusion, at least 0.1 nM of an ST receptor ligand per 10 kg bodyweight
XX CC per hour for at least 6 hours, where ST receptor ligand molecules bind to
XX CC ST receptors on the surface of the cancer cell in the individual and the
XX CC number of ST receptor molecules on the surface of the cancer cell is
XX CC increased. Therapeutic compositions comprising components which target ST
XX CC receptors can then be used to inhibit proliferation of the colorectal,
XX CC gastric and oesophageal cells. This method may be used for treating
XX CC individuals that have diseases that affect colorectal, gastric and
XX CC oesophageal cells, including colorectal, gastric or oesophageal cancers.
XX CC The present sequence represents a ST, designated ST 1b, which is used as
XX CC the ST receptor ligand in the method of the invention.
XX SQ Sequence 19 AA;

Query Match      100.0%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPACNGCY 19
Db 1 NSSNYCCCLCCNPACNGCY 19

RESULT 4
AAR85970
ID AAR85970 standard; peptide; 18 AA.
XX AC AAR85970;
XX DT 19-JAN-1996 (first entry)
XX DE ST 1b receptor ligand portion.
XX KW ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
XX KW colorectal; metastasis.
XX OS Escherichia coli.
XX PN WO9511694-A1.
XX PD 04-MAY-1995.
XX XX
```


PF 26-OCT-1994; 94WO-US012232.
 XX
 PR 26-OCT-1993; 93US-00141892.
 PR 13-SEP-1994; 94US-00305056.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Waldman SA;
 XX
 DR WPI; 1995-178646/23.
 XX
 PT Conjugated cpds. which specifically bind to colorectal cancer cells -
 PT comprise heat-stable toxin receptor binding moiety and active moiety
 PT which may be a therapeutic agent or a radioactive agent.
 XX
 PS Claim 3; Page 120; 133pp; English.
 XX
 CC New conjugated compounds are provided which consist of (1) an ST receptor
 CC binding moiety and (2) an active moiety which is a radio-stable agent.
 CC 'ST' refers to a heat stable toxin produced by E.coli and other
 CC organisms. Especially the radiostable agent is a therapeutic agent (e.g.
 CC methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive
 CC isotope) or nucleic acid; and the compound is used for the detection,
 CC imaging or treatment of colorectal tumours, particularly metastasised
 CC tumours. The present sequence is a specific example of an ST receptor
 CC binding peptide which can be used in the conjugate
 XX
 SQ Sequence 18 AA;
 Query Match 78.9%; Score 15; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NSSNYCCCLCCNPAC 15
 DB 1 NSSNYCCCLCCNPAC 15
 RESULT 5
 ID AAY40532
 AC AAY40532 standard; peptide; 18 AA.
 XX
 XX AAY40532;
 XX
 DT 03-DEC-1999 (first entry)
 XX
 DE ST receptor binding peptide.
 XX
 KW Conjugated compound; ST receptor; heat-stable; toxin; colorectal cancer.
 XX
 OS Escherichia coli.
 XX
 XX US962220-A.
 PN
 PD 05-OCT-1999.
 XX
 XX 06-JUN-1995; 95US-00467920.
 XX
 PR 26-OCT-1993; 93US-00141892.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 XX Waldman SA;
 PI
 DR WPI; 1999-571264/48.
 XX
 PT Conjugated compound comprising a receptor moiety and active moiety,
 PT useful for the treatment/prevention of colorectal cancer.
 XX
 PS Claim 1; Col 29-30; 23pp; English.
 XX
 CC The invention relates to a conjugated compound that comprises a ST (heat-
 CC stable toxin) receptor moiety selected from one of the sequences shown in
 CC

CC AAY40508-Y40559 and an active moiety (antisense molecule). The compound
 CC is useful for the treatment of colorectal cancer. The use of the
 CC conjugated compound is advantageous compared to antibodies since it binds
 CC specifically to colorectal cells and has no toxic effect on normal cells
 XX
 SQ Sequence 18 AA;
 Query Match 78.9%; Score 15; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NSSNYCCCLCCNPAC 15
 DB 1 NSSNYCCCLCCNPAC 15
 RESULT 6
 ID ADR45846
 XX ADR45846 standard; peptide; 18 AA.
 XX
 AC ADR45846;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Amino acid sequence of heat stable toxin ST 1b fragment.
 XX
 KW heat stable toxin; ST; ST receptor; colorectal cancer; gastric cancer;
 KW oesophageal cancer; colorectal cell; gastric cell; oesophageal cell;
 KW ST 1b.
 XX
 OS Unidentified.
 XX
 PN WO2004071436-A2.
 PD 26-AUG-2004.
 XX
 XX 10-FEB-2004; 2004WO-US003765.
 PF
 XX 10-FEB-2003; 2003US-0446730P.
 PR
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA
 XX Waldman SA, Pitari GM, Park J, Schulz S, Wolfe HR;
 PI
 DR WPI; 2004-615913/59.
 XX
 PT Increasing ST receptor molecules on the surface of a colorectal, gastric
 PT or oesophageal cancer cell to treat these cancers comprises administering
 PT ST receptor ligand molecules that bind to ST receptors on the surface of
 PT the cancer cell.
 XX
 PS Claim 6; SEQ ID NO 27; 97pp; English.
 XX
 CC The specification describes a method for increasing the number of heat
 CC stable toxin (ST) receptor molecules on the surface of a metastasised
 CC colorectal cancer cell. The method comprises administering, by continuous
 CC infusion, at least 0.1 nM of an ST receptor ligand per 10 kg bodyweight
 CC per hour for at least 6 hours, where ST receptor ligand molecules bind to
 CC ST receptors on the surface of the cancer cell in the individual and the
 CC number of ST receptor molecules on the surface of the cancer cell is
 CC increased. Therapeutic compositions comprising components which target ST
 CC receptors can then be used to inhibit proliferation of the colorectal,
 CC gastric and oesophageal cells. This method may be used for treating
 CC individuals that have diseases that affect colorectal, gastric and
 CC oesophageal cells, including colorectal, gastric or oesophageal cancers.
 CC The present sequence represents a fragment of a ST designated ST 1b (see
 CC ADR45825), which is used as the ST receptor ligand in the method of the
 CC invention.
 XX
 SQ Sequence 18 AA;
 Query Match 78.9%; Score 15; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
 DB 1 NSSNYCCCLCCNPAC 15

RESULT 7
 AAR95923
 ID AAR95923 standard; peptide; 19 AA.
 AC AAR95923;
 DT 14-JAN-1997 (first entry)
 DE Enterotoxigenic E. coli STa protein antigen.
 KW Mucosal binding composition; mucosal binding polypeptide; antigen;
 KW non-viral pathogen; sexually transmitted disease; administration;
 KW vaginal; rectal; oral; immune response; secretory immunity; mucous;
 KW enterotoxigenic; STa protein.
 XX Escherichia coli.
 OS WO9616178-A1.
 PN 30-MAY-1996.
 PD 17-NOV-1995; 95WO-GB002708.
 PF 17-NOV-1994; 94US-00342241.
 PR (LEBE/) LEBENS M R.
 PA (HOLM/) HOLMGREN J R.
 XX Lebens MR, Holmgren JR;
 PI WPI; 1996-268614/27.
 DR Mucosal binding compositions for generating mucosal immune response -
 PT comprises mucosal binding peptide, pref. derived from cholera toxin, and
 PT an antigen, e.g. derived from E. coli, HIV, etc.
 XX Claim 36; Page 44; 65pp; English.
 PS A novel mucosal binding compen. (MBC) comprises a mucosal binding
 CC polypeptide linked to at least 1 antigen from a non-viral pathogen, which
 CC causes a sexually transmitted disease (STD), e.g. the present
 CC enterotoxigenic E. coli STa protein antigen. The MBC, which is
 CC administered vaginally, rectally or orally, generates a mucosal immune
 CC response against the viral STD by allowing for the prodn. of high levels
 CC of secretory immunity, which forms the 1st line of defence against the
 CC majority of STD
 XX Sequence 19 AA;

Query Match 78.9%; Score 15; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.2e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 NSSNYCCCLCCNPAC 15
 DB 1 NSSNYCCCLCCNPAC 15

RESULT 8
 AAY02386
 ID AAY02386 standard; peptide; 19 AA.
 AC AAY02386;
 DT 09-JUL-1999 (first entry)
 DE Enterotoxigenic E. coli STa protein antigen.
 KW Mucosal binding composition; mucosal binding polypeptide; antigen;
 KW non-viral pathogen; sexually transmitted disease; administration;
 KW vaginal; rectal; oral; immune response; secretory immunity; mucous;
 KW enterotoxigenic; STa protein.
 XX Escherichia coli.
 OS WO9616178-A1.
 PN 30-MAY-1996.
 PD 17-NOV-1995; 95WO-GB002708.
 PF 17-NOV-1994; 94US-00342241.
 PR (LEBE/) LEBENS M R.
 PA (HOLM/) HOLMGREN J R.
 XX Lebens MR, Holmgren JR;
 PI WPI; 1996-268614/27.
 DR Mucosal binding compositions for generating mucosal immune response -
 PT comprises mucosal binding peptide, pref. derived from cholera toxin, and
 PT an antigen, e.g. derived from E. coli, HIV, etc.
 XX Claim 36; Page 44; 65pp; English.
 PS A novel mucosal binding compen. (MBC) comprises a mucosal binding
 CC polypeptide linked to at least 1 antigen from a non-viral pathogen, which
 CC causes a sexually transmitted disease (STD), e.g. the present
 CC enterotoxigenic E. coli STa protein antigen. The MBC, which is
 CC administered vaginally, rectally or orally, generates a mucosal immune
 CC response against the viral STD by allowing for the prodn. of high levels
 CC of secretory immunity, which forms the 1st line of defence against the
 CC majority of STD
 XX Sequence 19 AA;

Query Match 78.9%; Score 15; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.2e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 NSSNYCCCLCCNPAC 15
 DB 1 NSSNYCCCLCCNPAC 15

RESULT 9
 AAY29608
 ID AAY29608 standard; peptide; 19 AA.
 AC AAY29608;
 DT 15-OCT-1999 (first entry)
 DE Escherichia coli heat stable ST enterotoxin STH.
 KW Heat stable ST enterotoxin; immunoreagent; radiological therapy;
 KW diagnosis; ST receptor binding moiety; macrocyclic complexing agent;
 KW tumour; infectious diarrhoeal disease; diarrhoea.
 XX Escherichia coli.
 OS WO9939748-A1.
 PN 12-AUG-1999.
 PD 08-FEB-1999; 99WO-GB000396.
 PF 08-FEB-1999; 99WO-GB000396.
 XX

DE Heat stable ST enterotoxin Sth.
 XX Selection; candidate drug; cell receptor binding; affinity;
 KW biological receptor; rational drug design; combinatorial drug design;
 KW receptor antagonist; receptor agonist; ST enterotoxin; beta turn mimetic;
 KW gamma-turn mimetic; beta sheet mimetic; disulphide bridge mimetic.
 XX Escherichia coli.
 OS WO9909416-A2.
 PN 25-FEB-1999.
 PD 20-AUG-1998; 98WO-GB002504.
 PF 20-AUG-1997; 97GB-00017652.
 PR (NYCO-) NYCOMED IMAGING AS.
 PA (COCK/) COCKBAIN J.
 XX Wolfe HR;
 PI WPI; 1999-181156/15.
 DR Method of drug selection - and use of an acetamidomethyl-protected
 PT polymer as a substrate in the solid state synthesis of an oligopeptide.
 XX Disclosure; Page 1-2; 38pp; English.
 PS The specification describes a method for selecting a candidate drug
 CC compound having affinity for biological receptors. The method uses a
 CC combination of rational and combinatorial drug design techniques. At
 CC least 1 residue in the original cell receptor binding peptide is modified
 CC to a non-natural amino acid, preferably a beta turn mimetic, a gamma-turn
 CC mimetic, a beta sheet mimetic or a disulphide bridge mimetic. The method
 CC is used for identification of a candidate receptor antagonist or agonist.
 CC The present peptide is a cell receptor binding peptide, and can thus be
 CC used as a starting point for identification of candidate drug compounds,
 CC using the method of the invention
 XX Sequence 19 AA;

Query Match 78.9%; Score 15; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.2e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
 DB 1 NSSNYCCCLCCNPAC 15

RESULT 9
 AAY29608
 ID AAY29608 standard; peptide; 19 AA.
 AC AAY29608;
 DT 15-OCT-1999 (first entry)
 DE Escherichia coli heat stable ST enterotoxin STH.
 KW Heat stable ST enterotoxin; immunoreagent; radiological therapy;
 KW diagnosis; ST receptor binding moiety; macrocyclic complexing agent;
 KW tumour; infectious diarrhoeal disease; diarrhoea.
 XX Escherichia coli.
 OS WO9939748-A1.
 PN 12-AUG-1999.
 PD 08-FEB-1999; 99WO-GB000396.
 PF 08-FEB-1999; 99WO-GB000396.
 XX

PR 06-FEB-1998; 98US-00020233.
 XX (NYCO-) NYCOMED IMAGING AS.
 PA (MATT/) MATTHEWS D P.
 XX
 XX Snow RA, Delecki DJ, Shah C, Black C, Wolfe H;
 PI WPI; 1999-494219/41.
 XX
 XX Macrocytic complexing agents containing linked 2,6-pyridinylene nuclei
 PT as components of targeting immunoreagents binding to ST receptor.
 XX
 XX Disclosure; Page 39; 79pp; English.
 XX
 XX The present invention describes targeting immunoreagents (TI's)
 CC comprising a metal ion and a residue of a macrocyclic complexing agent
 CC (MCA). TI's are of use in diagnostic imaging and therapy of specific
 CC disease sites in a patient, using either radioactive, magnetic resonance,
 CC or fluorescent means of detection or use of the metal ion; alternatively,
 CC a substituent of these types may be introduced, e.g. radioactive iodine,
 CC to perform the same function. Most notable is the imaging and
 CC radiological therapy of tumours. In addition, a variety of bacteria,
 CC including Escherichia coli, Vibrio cholerae, Citrobacter freundii, and
 CC Yersinia enterocolitica, bind to ST receptors and cause infectious
 CC diarrhoeal diseases, particularly in pediatrics and in developing
 CC countries. These types of diarrhoea can also be treated using TI's. TI's
 CC may specifically used to treat cancers and also be used as an
 CC anti-diarrhoeal agent. TI's are free from the various disadvantages of
 CC prior art reagents, including rapid destruction and/or excretion,
 CC instability in storage, and protein degradation. There is no perturbation
 CC of protein reactive groups at the pyridyl chelating site. AAY29607 to
 CC AAY29612 represent examples of heat stable ST enterotoxins given in the
 CC exemplification of the present invention
 XX
 XX Sequence 19 AA;
 SQ

Query Match 78.9%; Score 15; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.2e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NSSNYCCCLCCNPAC 15
 DB 1 NSSNYCCCLCCNPAC 15
 |||||

RESULT 11
 AAY02398
 ID AAY02398 standard; peptide; 19 AA.
 XX
 AC AAY02398;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 DE Heat stable ST enterotoxin Sth.
 XX
 KW Selection; candidate drug; cell receptor binding; affinity;
 KW biological receptor; rational drug design; combinatorial drug design;
 KW receptor antagonist; receptor agonist; ST enterotoxin; beta turn mimetic;
 KW gamma-turn mimetic; beta sheet mimetic; disulphide bridge mimetic.
 XX
 OS Escherichia coli.
 XX
 PN WO9909417-A2.
 XX
 PD 25-FEB-1999.
 XX
 PF 20-AUG-1998; 98WO-GB002510.
 XX
 PR 20-AUG-1997; 97GB-00017652.
 XX
 XX (NYCO-) NYCOMED IMAGING AS.
 PA (COCK/) COCKBAIN J.
 XX
 PI Wolfe HR;
 XX
 XX WPI; 1999-181157/15.
 XX
 PT Method of drug selection - using a combination of rational and
 PT combinatorial drug design techniques.
 XX
 XX Disclosure; Page 1-2; 35pp; English.
 PS
 XX The specification describes a method for selecting a candidate drug
 CC

Query Match 78.9%; Score 15; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.2e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NSSNYCCCLCCNPAC 15
 DB 1 NSSNYCCCLCCNPAC 15
 |||||

RESULT 10
 AAY06972
 ID AAY06972 standard; peptide; 19 AA.
 XX
 AC AAY06972;
 XX
 DT 02-JUL-1999 (first entry)
 XX
 DE E. coli heat stable ST enterotoxin peptide Sth.
 XX
 KW Targeting immunoreagent; metal ion; immunoreactive; terpyridine; tumour;
 KW complexing agent; diagnostic imaging; radiological treatment; yttrium;
 KW therapeutic; radiation toxicity; heat stable; ST enterotoxin.
 XX
 OS Escherichia coli.
 XX
 PN WO9921587-A1.
 XX
 PD 06-MAY-1999.
 XX
 PF 15-OCT-1998; 98WO-GB003102.
 XX
 PR 15-OCT-1997; 97US-00951144.
 XX
 XX (NYCO-) NYCOMED IMAGING AS.
 PA (MATT/) MATTHEWS D P.
 XX
 XX Wolfe H, Delecki DJ, Yu S;
 PI

CC compound having affinity for biological receptors. The method uses a
CC combination of rational and combinatorial drug design techniques. At
CC least 1 residue in the original cell receptor binding peptide is modified
CC to a non-natural amino acid, preferably a beta turn mimetic, a gamma-turn
CC mimetic, a beta sheet mimetic or a disulfide bridge mimetic. The method
CC is used for identification of a candidate receptor antagonist or agonist.
CC The present peptide is a cell receptor binding peptide, and can thus be
CC used as a starting point for identification of candidate drug compounds,
CC using the method of the invention

XX
SQ Sequence 19 AA;
Query Match 78.9%; Score 15; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
DB 1 NSSNYCCCLCCNPAC 15
|||||

RESULT 12
AAM51879
ID AAM51879 standard; peptide; 19 AA.
AC AAM51879;
XX
XX
DT 01-FEB-2002 (first entry)
XX
DE Human thermostable enterotoxin Sth peptide fragment #3.
KW Human; thermostable enterotoxin; Sth; metastatic colorectal cancer;
KW guanyl cyclase-C; GC-C; Sth.
XX
XX Homo sapiens.
XX PR2805994-A1.
XX
XX 14-SEP-2001.
XX
PF 10-MAR-2000; 2000PR-00003141.
XX
XX 10-MAR-2000; 2000PR-00003141.
XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX
XX Der Vartanian M, Batisson I;
PI
XX WPI; 2001-640835/74.
XX
XX New compound for detecting and treating metastatic colorectal cancer
PT comprises a conjugate of an Sth peptide and an immunogenic protein which
PT binds to the guanyl cyclase-c receptor.
XX
XX Disclosure; Page 44; 126pp; French.
XX
XX The present invention relates to a conjugate which comprises an E. coli
CC thermostable enterotoxin (Sth) peptide and an active molecule where the
CC Sth peptide has a conformation such that it is capable of binding to the
CC guanyl cyclase-C (GC-C) receptor. This can be used in the specific
CC diagnosis and treatment of metastatic colorectal cancer. The present
CC sequence is a fragment of the human thermostable enterotoxin (Sth)
CC protein

XX
SQ Sequence 19 AA;
Query Match 78.9%; Score 15; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
DB 1 NSSNYCCCLCCNPAC 15
|||||

us-10-775-481a-5.olig.rag

CC compound having affinity for biological receptors. The method uses a
CC combination of rational and combinatorial drug design techniques. At
CC least 1 residue in the original cell receptor binding peptide is modified
CC to a non-natural amino acid, preferably a beta turn mimetic, a gamma-turn
CC mimetic, a beta sheet mimetic or a disulfide bridge mimetic. The method
CC is used for identification of a candidate receptor antagonist or agonist.
CC The present peptide is a cell receptor binding peptide, and can thus be
CC used as a starting point for identification of candidate drug compounds,
CC using the method of the invention

XX
SQ Sequence 19 AA;
Query Match 78.9%; Score 15; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
DB 1 NSSNYCCCLCCNPAC 15
|||||

RESULT 13
AAO16204
ID AAO16204 standard; peptide; 19 AA.
AC AAO16204;
XX
XX
DT 28-MAR-2003 (first entry)
XX
DE E coli small heat stable enterotoxin tricyclo peptide, SEQ ID No 23.
XX
KW Guanylate cyclase receptor agonist; apoptosis induction; cancer; polyps;
KW inflammation; asthma; nephritis; hepatitis; bronchitis; cystic fibrosis;
KW small heat stable enterotoxin tricyclo; inflammatory bowel disease;
KW pancreatitis; ulcerative colitis; Crohn's disease; Kaposi's sarcoma.
XX
XX Escherichia coli.
XX
XX Key Location/Qualifiers
FH Disulfide-bond 6..10
FT Disulfide-bond 7..15
FT Disulfide-bond 11..18
XX
XX WO200278683-A1.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009551.
XX
XX 29-MAR-2001; 2001US-0279437P.
PR 29-MAR-2001; 2001US-0279438P.
PR 27-JUN-2001; 2001US-0300850P.
PR 10-JUL-2001; 2001US-0303808P.
PR 25-JUL-2001; 2001US-0307358P.
PR 17-JAN-2002; 2002US-0348646P.
XX
XX (SYNE-) SYNERGY PHARM INC.
XX
XX Shailubhai K, Nikiforovich G, Jacob GS;
XX
XX WPI; 2003-148251/14.
XX
XX Novel guanylate cyclase receptor agonist peptide useful for preventing or
PT treating primary or metastatic cancer and polyps in a patient, and for
PT inducing apoptosis in the cells of a subject.
XX
XX Disclosure; Page 10; 47pp; English.
XX
XX The invention comprises guanylate cyclase receptor agonist peptides that
CC are useful for inducing apoptosis in the cells of a subject. The peptides
CC of the invention may be used to treat: cancer; polyps; inflammation;
CC asthma; nephritis; hepatitis; pancreatitis; bronchitis; cystic fibrosis;
CC inflammatory bowel disease; ulcerative colitis; Crohn's disease; and
CC Kaposi's sarcoma. The present amino acid sequence represents an
CC Escherichia coli small heat stable enterotoxin tricyclo peptide which was
CC used in the invention

XX
SQ Sequence 19 AA;
Query Match 78.9%; Score 15; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
DB 1 NSSNYCCCLCCNPAC 15
|||||

RESULT 14
ABG74825
ID ABG74825 standard; peptide; 19 AA.
XX

AC ABG74825;
XX 12-JUN-2003 (first entry)
XX DE E. coli heat stable enterotoxin derived peptide SEQ ID 7.
XX AC
KW Apical membrane; mucosal epithelial cell; respiratory tract;
KW guanylate cyclase C; G protein-coupled receptor; guanosine triphosphate;
KW cyclic guanosine monophosphate; cGMP; chloride ion secretion; inhalation;
KW membrane-associated type II protein kinase; mucus fluidisation;
KW cystic fibrosis transmembrane conductance regulator; breathing disorder;
KW mucus secretion; antiasthmatic; antiinflammatory; bronchial asthma;
KW chronic bronchitis; cystic fibrosis; enterotoxin; heat stable.
XX Escherichia coli.
OS
XX WO200298912-A2.
XX
XX PD 12-DEC-2002.
XX
XX PF 05-JUN-2002; 2002WO-DE002040.
XX
XX PR 05-JUN-2001; 2001DE-01027119.
XX
XX PA (CETI/) CETIN Y.
XX PA (SAVA/) SAVAS Y.
XX
XX PI Cetin Y, Savas Y;
XX
XX DR WPI; 2003-156842/15.
XX
XX PT Composition useful for treating respiratory disease, comprises a peptide
XX PT that activates guanylate cyclase C, and is delivered to the apical
XX PT membrane through the respiratory tract.
XX
XX PS Claim 3; Page 4; 23pp; German.
XX
XX CC This invention describes a novel medicament in a formulation that is
XX CC delivered to the apical membrane of mucosal epithelial cells through the
XX CC respiratory tract. The medicament contains at least one peptide that
XX CC activates guanylate cyclase C (GCC). GCC is a G protein-coupled receptor
XX CC that catalyses conversion of guanosine triphosphate to cyclic guanosine
XX CC monophosphate (cGMP) and is present on the apical (air) side of
XX CC respiratory epithelial cells but not on the basolateral (blood) side.
XX CC cGMP activates membrane-associated type II protein kinase which in turn
XX CC activates the regulatory domain of the cystic fibrosis transmembrane
XX CC conductance regulator, resulting in secretion of chloride ions and water
XX CC from the cells, causing fluidisation of the mucus. The products of the
XX CC invention are used to make an inhalation device containing the medicament
XX CC for diagnosing diseases that are accompanied by breathing disorders or
XX CC disorders of mucus secretion in the respiratory tract, by detecting at
XX CC least one GCC activator. The products of the invention have antiasthmatic
XX CC and antiinflammatory activity. The method is useful for diagnosing and
XX CC treating diseases accompanied by breathing disorders or disorders of
XX CC mucus secretion in the respiratory tract particularly bronchial asthma,
XX CC chronic bronchitis and cystic fibrosis. The product of the invention
XX CC improves fluidity and evacuation of bronchial mucus and acts locally
XX CC (since the medicament does not enter the bloodstream), so systemic side
XX CC effects are minimised. Only very small doses of the medicament are
XX CC required. This sequence represents a heat stable E. coli enterotoxin
XX CC derived peptide use in an assay to determine guanylate cyclase C
XX CC activation described in the disclosure of the invention
XX
SQ Sequence 19 AA;
Query Match 78.9%; Score 15; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NSSNYCCCLCCNPAC 15
Db 1 NSSNYCCCLCCNPAC 15
Search completed: March 26, 2005, 17:20:58
Job time : 85.4821 secs

RESULT 15
ADCI14120
ID ADCI14120 standard; peptide; 19 AA.
XX
XX AC ADCI14120;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DE Heat stable enterotoxin, STH.
XX
XX KW Breast cancer; prostate cancer; pancreatic cancer; melanoma;
KW heat stable enterotoxin; ST motif; tail region; receptor binding region;
KW cytotostatic.
XX
XX OS Escherichia coli.
XX
XX FH Key Location/Qualifiers
FT Disulfide-bond 6..11
FT Disulfide-bond 7..15
FT Disulfide-bond 10..18.
XX
XX PN WO2003072125-A1.
XX
XX PD 04-SEP-2003.
XX
XX PF 21-FEB-2003; 2003WO-US005343.
XX
XX PR 22-FEB-2002; 2002US-0359204P.
XX
XX PA (UMOR) UNIV MISSOURI.
XX
XX PI Sieckman G, Gali H, Volkert W, Forte L, Hoffman T;
XX
XX DR WPI; 2003-731571/69.
XX
XX PT Method of treating or preventing breast, prostate, pancreatic cancer or
XX PT melanoma, comprises targeting peptide agent complex to breast cancer
XX PT cell, prostate cancer cell, pancreatic cancer cell or melanoma cancer
XX PT cell.
XX
XX PS Disclosure; Fig 1; 4lpp; English.
XX
XX CC The present invention relates to a method for targeting an agent to a
XX CC breast cancer cell, prostate cancer cell, a pancreatic cancer cell or
XX CC melanoma cancer cell. The method involves contacting the cancer cell with
XX CC a peptide agent complex wherein the peptide comprises an E. coli heat
XX CC stable enterotoxin (ST) motif that binds to the cancer cell. The ST motif
XX CC may comprise a tail region (ADCI14118) and an receptor binding region
XX CC (ADCI14119). The method is used for targeting an agent to breast,
XX CC prostate, pancreatic or melanoma cancer cell; for rendering, treating and
XX CC preventing an unresectable breast, prostate, pancreatic or melanoma
XX CC tumour and for identifying tumour binding peptide. The present sequence
XX CC is heat stable enterotoxin (STH) produced by human strain of Escherichia
XX CC coli bacteria.
XX
SQ Sequence 19 AA;
Query Match 78.9%; Score 15; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NSSNYCCCLCCNPAC 15
Db 1 NSSNYCCCLCCNPAC 15

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OM protein - protein search, using sw model

Run on: March 26, 2005, 17:12:01 ; Search time 25.7857 Seconds
(without alignments)
55.005 Million cell updates/sec

Title: US-10-775-481A-5

Perfect score: 19

Sequence: 1 NSSNYCCELCCNPACNGCY 19

Scoring table: 

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	1	US-08-141-892A-5
2	19	100.0	19	2	US-08-583-447A-5
3	19	100.0	19	2	US-08-467-920-5
4	19	100.0	19	3	US-08-635-930-5
5	19	100.0	19	3	US-09-193-997-5
6	19	100.0	19	3	US-09-138-237A-5
7	15	78.9	18	1	US-08-141-892A-27
8	15	78.9	18	2	US-08-583-447A-27
9	15	78.9	18	2	US-08-467-920-27
10	15	78.9	18	3	US-08-635-930-27
11	15	78.9	18	3	US-09-193-997-27
12	15	78.9	18	3	US-09-138-237A-27
13	14	73.7	17	1	US-08-141-892A-28
14	14	73.7	17	2	US-08-583-447A-28
15	14	73.7	17	2	US-08-467-920-28
16	14	73.7	17	3	US-08-635-930-28
17	14	73.7	17	3	US-09-193-997-28
18	14	73.7	17	3	US-09-138-237A-28
19	14	73.7	18	1	US-08-141-892A-33
20	14	73.7	18	2	US-08-583-447A-33
21	14	73.7	18	2	US-08-467-920-33
22	14	73.7	18	3	US-08-635-930-33
23	14	73.7	18	3	US-09-193-997-33
24	14	73.7	18	3	US-09-138-237A-33
25	13	68.4	16	1	US-08-141-892A-29
26	13	68.4	16	2	US-08-583-447A-29
27	13	68.4	16	2	US-08-467-920-29

28	13	68.4	16	3	US-08-635-930-29	Sequence 29, Appl
29	13	68.4	16	3	US-09-193-997-29	Sequence 29, Appl
30	13	68.4	16	3	US-09-138-237A-29	Sequence 29, Appl
31	13	68.4	17	1	US-08-141-892A-34	Sequence 34, Appl
32	13	68.4	17	2	US-08-583-447A-34	Sequence 34, Appl
33	13	68.4	17	2	US-08-467-920-34	Sequence 34, Appl
34	13	68.4	17	3	US-08-635-930-34	Sequence 34, Appl
35	13	68.4	17	3	US-09-193-997-34	Sequence 34, Appl
36	13	68.4	17	3	US-09-138-237A-34	Sequence 34, Appl
37	12	63.2	15	1	US-08-141-892A-30	Sequence 30, Appl
38	12	63.2	15	2	US-08-583-447A-30	Sequence 30, Appl
39	12	63.2	15	2	US-08-467-920-30	Sequence 30, Appl
40	12	63.2	15	3	US-08-635-930-30	Sequence 30, Appl
41	12	63.2	15	3	US-09-193-997-30	Sequence 30, Appl
42	12	63.2	15	3	US-09-138-237A-30	Sequence 30, Appl
43	12	63.2	16	1	US-08-141-892A-35	Sequence 35, Appl
44	12	63.2	16	2	US-08-583-447A-35	Sequence 35, Appl
45	12	63.2	16	2	US-08-467-920-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-08-141-892A-5
; Sequence 5, Application US/08141892A
; Patent No. 5518888
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
; TITLE OF INVENTION: of Using the Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,892A
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0903
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-141-892A-5

Query Match 100.0%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSSNYCCELCCNPACNGCY 19
Db 1 NSSNYCCELCCNPACNGCY 19

RESULT 2
US-08-583-447A-5
; Sequence 5, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-583-447A-5
Query Match 100.0%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NSSNYCCCLCCNPACNGCY 19
Db 1 NSSNYCCCLCCNPACNGCY 19

RESULT 3
US-08-467-920-5
; Sequence 5, Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,920
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1589
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-920-5
Query Match 100.0%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NSSNYCCCLCCNPACNGCY 19
Db 1 NSSNYCCCLCCNPACNGCY 19

RESULT 4
US-08-635-930-5
; Sequence 5, Application US/08635930
; Patent No. 6060037
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically Bind To
; Colorectal Cancer Cells And Methods Of Using
; TITLE OF INVENTION: The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WordPerfect 6.0/6.1
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; APPLICATION NUMBER: US/08/635,930
; FILING DATE: 26-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,056
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark

REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1360
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-635-930-5

Query Match 100.0%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPACNGCY 19
Db 1 NSSNYCCCLCCNPACNGCY 19

RESULT 5

US-09-193-997-5
Sequence 5, Application US/09193997
Patent No. 6087109

GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically
Bind To Colorectal Cancer Cells
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 6087109ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,997
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,920
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1589
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-193-997-5

Query Match 100.0%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPACNGCY 19

Db 1 NSSNYCCCLCCNPACNGCY 19

RESULT 6

US-09-138-237A-5
Sequence 5, Application US/09138237A
Patent No. 6268159

GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: Of Using the Same
NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6268159ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,237A
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-138-237A-5

Query Match 100.0%; Score 19; DB 3; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.3e-13;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPACNGCY 19

Db 1 NSSNYCCCLCCNPACNGCY 19

RESULT 7

US-08-141-892A-27

Sequence 27, Application US/08141892A
Patent No. 5518888

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: Of Using the Same
NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,892A
FILING DATE: 26-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-141-892A-27

Query Match 78.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
DB 1 NSSNYCCCLCCNPAC 15

RESULT 8

US-08-583-447A-27
Sequence 27, Application US/08583447A
Patent No. 5879656
GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: St Receptor Binding Compounds and
METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-583-447A-27

Query Match 78.9%; Score 15; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
DB 1 NSSNYCCCLCCNPAC 15

RESULT 9

US-08-467-920-27
Sequence 27, Application US/08467920
Patent No. 5962220
GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically
Bind To Colorectal Cancer Cells
METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,920
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1589
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-467-920-27

Query Match 78.9%; Score 15; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
DB 1 NSSNYCCCLCCNPAC 15

RESULT 10

US-08-635-930-27
Sequence 27, Application US/08635930

Patent No. 6060037
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically Bind To
; TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using
; TITLE OF INVENTION: The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WordPerfect 6.0/6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,930
; FILING DATE: 26-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,056
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1360
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-635-930-27

Query March 78.9%; Score 15; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPAC 15
Db 1 NSSNYCCCLCCNPAC 15

RESULT 11
US-09-193-997-27
; Sequence 27, Application US/09193997
; Patent No. 6087109
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/193,997
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/467,920
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-193-997-27

Query March 78.9%; Score 15; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPAC 15
Db 1 NSSNYCCCLCCNPAC 15

RESULT 12
US-09-138-237A-27
; Sequence 27, Application US/09138237A
; Patent No. 6268159
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: St Receptor Binding Compounds and Methods
; TITLE OF INVENTION: of Using the Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6268159ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,237A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0903
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-138-237A-27

Query Match 78.9%; Score 15; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
Db 1 NSSNYCCCLCCNPAC 15

RESULT 13

US-08-141-892A-28
Sequence 28, Application US/08141892A
Patent No. 5518888
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: Of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,892A
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-141-892A-28

Query Match 73.7%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNYCCCLCCNPAC 15
Db 1 SSNYCCCLCCNPAC 14

RESULT 14

US-08-583-447A-28
Sequence 28, Application US/08583447A
Patent No. 5879656
GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
TITLE OF INVENTION: Methods of Using the Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-583-447A-28

Query Match 73.7%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNYCCCLCCNPAC 15
Db 1 SSNYCCCLCCNPAC 14

RESULT 15

US-08-467-920-28
Sequence 28, Application US/08467920
Patent No. 5962220
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5962220ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,920

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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-467-920-28

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Query Match      73.7%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 SSNYCCCLCCNPAC 14

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Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2005, 17:25:02 ; Search time 61.4107 Seconds
(without alignments)
102.440 Million cell updates/sec

Title: US-10-775-481A-5

Perfect score: 19

Sequence: 1 NSSNYCCELCNACNGCY 19

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1407402 seqs, 331100923 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpaa/FCT_NEW_PUB.pep.*
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- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	15	78.9	19	15	US-10-371-966-1
5	15	78.9	19	15	US-10-371-966-2
6	15	78.9	19	17	US-10-796-719-1
7	15	78.9	19	17	US-10-796-719-26
8	15	78.9	19	17	US-10-796-719-27
9	15	78.9	19	17	US-10-479-606-7
10	15	78.9	21	17	US-10-796-719-39
11	15	78.9	21	17	US-10-796-719-40
12	15	78.9	72	17	US-10-796-719-21
13	14	73.7	17	15	US-10-621-684-28

14	73.7	18	15	US-10-621-684-33	Sequence 33, Appl
15	68.4	16	15	US-10-621-684-29	Sequence 29, Appl
16	68.4	17	15	US-10-621-684-34	Sequence 34, Appl
17	63.2	15	15	US-10-621-684-30	Sequence 30, Appl
18	63.2	15	15	US-10-621-684-35	Sequence 35, Appl
19	57.9	14	15	US-10-621-684-11	Sequence 11, Appl
20	57.9	14	15	US-10-621-684-31	Sequence 31, Appl
21	57.9	14	15	US-10-621-684-43	Sequence 43, Appl
22	57.9	15	15	US-10-621-684-10	Sequence 10, Appl
23	57.9	15	15	US-10-621-684-16	Sequence 16, Appl
24	57.9	15	15	US-10-621-684-36	Sequence 36, Appl
25	57.9	15	15	US-10-621-684-42	Sequence 42, Appl
26	57.9	16	15	US-10-621-684-9	Sequence 9, Appl
27	57.9	16	15	US-10-621-684-15	Sequence 15, Appl
28	57.9	17	15	US-10-621-684-8	Sequence 8, Appl
29	57.9	17	15	US-10-621-684-14	Sequence 14, Appl
30	57.9	18	15	US-10-621-684-41	Sequence 41, Appl
31	57.9	18	15	US-10-621-684-7	Sequence 7, Appl
32	57.9	18	15	US-10-621-684-13	Sequence 13, Appl
33	57.9	18	15	US-10-621-684-38	Sequence 38, Appl
34	57.9	18	17	US-10-796-719-2	Sequence 2, Appl
35	57.9	18	17	US-10-796-719-4	Sequence 4, Appl
36	57.9	18	17	US-10-796-719-11	Sequence 11, Appl
37	57.9	19	15	US-10-621-684-2	Sequence 2, Appl
38	57.9	19	15	US-10-621-684-49	Sequence 49, Appl
39	57.9	72	17	US-10-796-719-20	Sequence 20, Appl
40	52.6	13	15	US-10-621-684-12	Sequence 12, Appl
41	52.6	13	15	US-10-621-684-32	Sequence 32, Appl
42	52.6	13	15	US-10-621-684-45	Sequence 45, Appl
43	52.6	14	15	US-10-621-684-17	Sequence 17, Appl
44	52.6	14	15	US-10-621-684-37	Sequence 37, Appl
45	52.6	14	15	US-10-621-684-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1

US-10-621-684-5
; Sequence 5, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods of Using the Same

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris

STREET: One Liberty Place, 46th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows

SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/621,684

FILING DATE: 17-Jul-2003

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/583,447A

FILING DATE: 05-JAN-1996

APPLICATION NUMBER: US 08/141,892

FILING DATE: 26-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: DeLuca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-1702

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-621-684-5

Query Match 100.0%; Score 19; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
DB 1 NSSNYCCCLCCNPACNGCY 19

RESULT 2
US-10-621-684-27
; Sequence 27, Application US/10621694
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621.684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583.447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-621-684-27

Query Match 78.9%; Score 15; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
DB 1 NSSNYCCCLCCNPAC 15

RESULT 3
US-10-107-814-23
; Sequence 23, Application US/10107814
; Publication No. US20030073628A1
; GENERAL INFORMATION:
; APPLICANT: SHAILUBHAI, KUNWAR
; APPLICANT: NIKIFOROVICH, GREGORY
; APPLICANT: JACOB, GARY S.
; TITLE OF INVENTION: GUANYLATE CYCLASE RECEPTOR AGONISTS FOR THE TREATMENT
; OF TISSUE INFLAMMATION AND CARCINOGENESIS
; FILE REFERENCE: 81361/284943/MAS
; CURRENT APPLICATION NUMBER: US/10/107.814
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (6)..(10)
; NAME/KEY: DISULFID
; LOCATION: (7)..(15)
; NAME/KEY: DISULFID
; LOCATION: (11)..(18)
US-10-107-814-23

Query Match 78.9%; Score 15; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
DB 1 NSSNYCCCLCCNPAC 15

RESULT 4
US-10-371-966-1
; Sequence 1, Application US/10371966
; Publication No. US20030232013A1
; GENERAL INFORMATION:
; APPLICANT: SIECKMAN, GARY
; APPLICANT: VOLKERT, WYNN
; APPLICANT: FORTE, LEONARD
; APPLICANT: HOFFMAN, TIMOTHY
; APPLICANT: GALLI, HARIPRASAD
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TARGETING OF CANCERS CELLS
; TITLE OF INVENTION: WITH TUMOR HOMING PEPTIDES
; FILE REFERENCE: UVM0:013US
; CURRENT APPLICATION NUMBER: US/10/371.966
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/359,204
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-371-966-1

Query Match 78.9%; Score 15; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
DB 1 NSSNYCCCLCCNPAC 15

```
RESULT 5
US-10-371-966-2
; Sequence 2, Application US/10371966
; Publication No. US20030232013A1
; GENERAL INFORMATION:
; APPLICANT: SIECKMAN, GARY
; APPLICANT: VOLKERT, WYNN
; APPLICANT: FORTE, LEONARD
; APPLICANT: HOFFMAN, TIMOTHY
; APPLICANT: GALI, HARIPRASAD
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TARGETING OF CANCERS CELLS
; TITLE OF INVENTION: WITH TUMOR HOMING PEPTIDES
; FILE REFERENCE: UWMO:01305
; CURRENT APPLICATION NUMBER: US/10/371,966
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/359,204
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-371-966-2

Query Match      78.9%; Score 15; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NSSNYCCCLCCNPAC 15
Db      1 NSSNYCCCLCCNPAC 15

RESULT 6
US-10-796-719-1
; Sequence 1, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-796-719-1

Query Match      78.9%; Score 15; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NSSNYCCCLCCNPAC 15
Db      1 NSSNYCCCLCCNPAC 15

RESULT 7
US-10-796-719-2
; Sequence 26, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-2

Query Match      78.9%; Score 15; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NSSNYCCCLCCNPAC 15
Db      1 NSSNYCCCLCCNPAC 15

RESULT 8
US-10-796-719-27
; Sequence 27, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-27

Query Match      78.9%; Score 15; DB 17; Length 19;
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Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
   |||||
Db 1 NSSNYCCCLCCNPAC 15

RESULT 9
US-10-479-606-7
; Sequence 7, Application US/10479606
; Publication No. US20050032684A1
; GENERAL INFORMATION:
; APPLICANT: Savas, Yukeel
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: Guanylate-cyclase C ligand, administered via the airways, for the
; FILE REFERENCE: 03100192aa
; CURRENT APPLICATION NUMBER: US/10/479,606
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: DE10127119.0
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/DE02/02040
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-479-606-7

Query Match 78.9%; Score 15; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
   |||||
Db 1 NSSNYCCCLCCNPAC 15

RESULT 10
US-10-796-719-39
; Sequence 39, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-39

Query Match 78.9%; Score 15; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
   |||||
Db 1 NSSNYCCCLCCNPAC 15

RESULT 11
US-10-796-719-40
; Sequence 40, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-40

Query Match 78.9%; Score 15; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
   |||||
Db 1 NSSNYCCCLCCNPAC 15

RESULT 12
US-10-796-719-21
; Sequence 21, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-796-719-21
```

```
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
   |||||
Db 1 NSSNYCCCLCCNPAC 15

RESULT 11
US-10-796-719-40
; Sequence 40, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-40

Query Match 78.9%; Score 15; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPAC 15
   |||||
Db 1 NSSNYCCCLCCNPAC 15

RESULT 12
US-10-796-719-21
; Sequence 21, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-796-719-21
```

Query Match 78.9%; Score 15; DB 17; Length 72;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPAC 15
Db 54 NSSNYCCCLCCNPAC 68

RESULT 13

US-10-621-684-28
; Sequence 28, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/593,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993

ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-10-621-684-28

Query Match 73.7%; Score 14; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NSSNYCCCLCCNPAC 15
Db 1 NSSNYCCCLCCNPAC 14

RESULT 14

US-10-621-684-33
; Sequence 33, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/593,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993

ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-621-684-33

Query Match 73.7%; Score 14; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NSSNYCCCLCCNPAC 15
Db 1 NSSNYCCCLCCNPAC 14

RESULT 15

US-10-621-684-29
; Sequence 29, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-621-684-29

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Query Match      68.4%; Score 13; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      3 SNYCCELCCNPAC 15
Db      1 SNYCCELCCNPAC 13

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Search completed: March 26, 2005, 17:44:31
Job time : 61.4107 secs

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OM protein - protein search, using sw model

Run on: March 26, 2005, 17:10:31 ; Search time 19.6786 Seconds
(without alignments)
92.899 Million cell updates/sec

Title: US-10-775-481A-5
Perfect score: 19
Sequence: 1 NSSNYCCCLCCNPACNGCY 19
Scoring table:  Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues
Word size : 0
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	78.9	72	1 QHEC4	heat-stable entero
2	15	78.9	72	1 QHEC1B	heat-stable entero
3	11	57.9	18	2 A60103	heat-stable entero
4	11	57.9	72	1 QHEC1	heat-stable entero
5	10	52.6	53	2 S68705	heat-stable entero
6	7	36.8	18	1 QHEC2	heat-stable entero
7	7	36.8	248	2 T19913	hypothetical prote
8	6	31.6	13	2 A28953	alpha-conotoxin SI
9	6	31.6	15	1 N7KNAG	alpha-conotoxin GI
10	6	31.6	17	2 A54534	heat-stable entero
11	6	31.6	19	2 A44379	alpha-conotoxin SI
12	6	31.6	65	2 S34671	heat-stable entero
13	6	31.6	66	2 S31652	enterotoxin - Vers
14	6	31.6	71	2 S25659	heat-stable entero
15	6	31.6	78	1 QHVC1	heat-stable entero
16	6	31.6	124	1 NRPGB	pancreatic ribonuc
17	6	31.6	128	1 NRPGB	pancreatic ribonuc
18	6	31.6	136	2 T16269	hypothetical prote
19	6	31.6	408	2 T37929	probable major fac
20	6	31.6	796	2 T20091	hypothetical prote
21	5	26.3	75	2 H84631	hypothetical prote
22	5	26.3	90	2 D85845	probable lysis pro
23	5	26.3	110	2 I74319	gene EHS-2 protein
24	5	26.3	116	2 S77004	umuC protein - Syn
25	5	26.3	118	2 D97733	hypothetical prote
26	5	26.3	122	1 NRKGR	pancreatic ribonuc
27	5	26.3	124	1 NRBOB	pancreatic ribonuc
28	5	26.3	124	1 NRANE	pancreatic ribonuc
29	5	26.3	124	1 NRDEF	pancreatic ribonuc

30	5	26.3	124	1 NRDEN	pancreatic ribonuc
31	5	26.3	124	1 NRDEO	pancreatic ribonuc
32	5	26.3	124	1 NRDER	pancreatic ribonuc
33	5	26.3	124	1 NREKN	pancreatic ribonuc
34	5	26.3	124	1 NRGF	pancreatic ribonuc
35	5	26.3	124	1 NRGN	pancreatic ribonuc
36	5	26.3	124	1 NRGT	pancreatic ribonuc
37	5	26.3	124	1 NRPBH	pancreatic ribonuc
38	5	26.3	124	1 NRSH	pancreatic ribonuc
39	5	26.3	124	1 NRWB	pancreatic ribonuc
40	5	26.3	124	2 S07141	pancreatic ribonuc
41	5	26.3	124	2 S08547	pancreatic ribonuc
42	5	26.3	124	2 S08546	pancreatic ribonuc
43	5	26.3	124	2 S08549	pancreatic ribonuc
44	5	26.3	124	2 C96762	hypothetical prote
45	5	26.3	125	2 A86872	transcription regu

ALIGNMENTS

RESULT 1

QHEC4
heat-stable enterotoxin STA4 precursor - Escherichia coli
C:Species: Escherichia coli
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JT0373; A35978
R:Stieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.;
Plasmid 20, 42-53, 1988
A:Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escheri
A:Reference number: JT0373; MUID:89202548; PMID:3071819
A:Accession: JT0373
A:Molecule type: DNA
A:Residues: 1-72 <STI>
A:Cross-references: UNIPROT:P07965; GB:J03311; MID:9147875; PIDN:AAA24652.1; PID:9147876
T:Zhou, X.; Shen, L.P.; Chi, C.W.
Toxicon 28, 453-456, 1990
A:Title: Isolation and nucleotide sequence determination of a gene encoding a heat-stabl
A:Reference number: A35978; MUID:90273381; PMID:2190361
A:Accession: A35978
A:Molecule type: DNA
A:Residues: 1-72 <ZHO>
C:Genetics:
A:Gene: estA4
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:1-19/Domain: signal sequence #status Predicted <SIG>
F:20-53/Domain: propeptide #status Predicted <PRO>
F:54-72/Product: heat-stable enterotoxin #status Predicted <MAT>
F:59-64,60-68,63-71/Disulfide bonds: #status Predicted

Query Match 78.9% Score 15; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.9e+10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPAC 15
Db 54 NSSNYCCCLCCNPAC 68
|||||

RESULT 2

QHEC1B
heat-stable enterotoxin ST-1b precursor - Escherichia coli
N:Alternate names: heat-stable enterotoxin ST-A2
C:Species: Escherichia coli
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C:Accession: JS0292; A33067; A30567
R:Moseley, S.L.; Hardy, J.W.; Huq, M.I.; Echeverria, P.; Falkow, S.
Infect. Immun. 39, 1167-1174, 1983
A:Title: Isolation and nucleotide determination of a gene encoding a heat-stable enteroto
A:Reference number: JS0292; MUID:83184648; PMID:6341230
A:Accession: JS0292
A:Molecule type: DNA

A;Residues: 1-72 <WOS>
 A;Cross-references: UNIPROT:Q47185; UNIPROT:P07965; GB:M34916; NID:gl46407; PIDN:AAA23099
 R;Dwarakanath, P.; Valsweswarian, S.S.; Subrahmanyam, Y.V.B.K.; Shanthi, G.; Jagannatha, Gene 81, 219-226, 1989
 A;Title: Cloning and hyperexpression of a gene encoding the heat-stable toxin of *Escherichia coli* serotype O157:H7
 A;Reference number: A33068; MUID:90034194; PMID:2680769
 A;Accession: A33068
 A;Molecule type: DNA
 A;Residues: 1-18, 'A', 20-72 <DWA>
 A;Cross-references: GB:M29255; NID:gl48029; PIDN:AAA24686.1; PID:gl48030
 A;Note: the authors translated the codon AAG for residue 2 as Val and CTA for residue 34
 R;Almota, S.; Takao, T.; Shimonishi, Y.; Hara, S.; Takeda, T.; Takeda, Y.; Miwatani, T. Eur. J. Biochem. 129, 257-263, 1982
 A;Title: Amino acid sequence of heat-stable enterotoxin produced by human enterotoxigenic *Escherichia coli* serotype O157:H7
 A;Reference number: A33067; MUID:83105138; PMID:6759126
 A;Accession: A33067
 A;Molecule type: protein
 A;Residues: 54-72 <AIM>
 R;Guzman-Verduzco, L.M.; Kuperstoch, Y.M. Infect. Immun. 57, 645-648, 1989
 A;Title: Rectification of two *Escherichia coli* heat-stable enterotoxin allele sequences
 A;Reference number: A30567; MUID:89108616; PMID:2643580
 A;Accession: A30567
 A;Molecule type: DNA
 A;Residues: 1-18, 'A', 20-24, 'AG', 27-41, 'V', 43-44, 'N', 46, 'E', 48, 'S', 50-72 <GUZ>
 A;Cross-references: GB:M18345; NID:gl45862; PIDN:AAA23729.1; PID:gl45863
 A;Comment: This is one of the type I heat-stable enterotoxins that are methanol-soluble.
 C;Genetics:
 A;Gene: st
 C;Superfamily: heat-stable enterotoxin ST
 C;Keywords: enterotoxin; heat-stable protein
 F;1-53/Domain: signal sequence and propeptide #status predicted <SIG>
 F;54-72/Product: heat-stable enterotoxin ST-Ib #status experimental <MAT>
 F;59-64,60-68,63-71/Disulfide bonds: #status experimental

Query Match 78.9%; Score 15; DB 1; Length 72;
 Best Local Similarity 100.0%; Pred. No. 1.9e-10;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCELCCNPAC 15
 |||||
 DB 54 NSSNYCCELCCNPAC 68

RESULT 3
 A60103
 heat-stable enterotoxin ST-Ia - *Citrobacter freundii*
 C;Species: *Citrobacter freundii*
 C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
 C;Accession: A60103
 R;Guarino, A.; Giannella, R.; Thompson, M.R. Infect. Immun. 57, 649-652, 1989
 A;Title: *Citrobacter freundii* produces an 18-amino-acid heat-stable enterotoxin identical to *Escherichia coli* serotype O157:H7
 A;Reference number: A60103; MUID:89108617; PMID:2912902
 A;Accession: A60103
 A;Molecule type: protein
 A;Residues: 1-18 <GUA>
 A;Cross-references: UNIPROT:Q7M0U3
 C;Superfamily: heat-stable enterotoxin ST

Query Match 57.9%; Score 11; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.6e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YCCELCCNPAC 15
 |||||
 DB 4 YCCELCCNPAC 14

RESULT 4
 QHSC1
 heat-stable enterotoxin ST-I precursor - *Escherichia coli*
 N;Alternate names: heat-stable enterotoxin estA1

C;Species: *Escherichia coli*
 C;Date: 31-Aug-1980 #sequence_revision 31-Aug-1980 #text_change 09-Jul-2004
 C;Accession: A01822; A30985; A36732; JT0374; I51932
 R;SO, M.; McCarthy, B.J. Proc. Natl. Acad. Sci. U.S.A. 77, 4011-4015, 1980
 A;Title: Nucleotide sequence of the bacterial transposon Tn1681 encoding a heat-stable (ST) enterotoxin
 A;Reference number: A01822; MUID:81054703; PMID:6254008
 A;Accession: A01822
 A;Molecule type: DNA
 A;Residues: 1-72 <LAZ>
 A;Cross-references: UNIPROT:P01559; GB:V00612; GB:J01831; NID:gl43704; PIDN:CAA23883.1; R;Lazure, C.; Seidah, N.G.; Chretien, M.; Lallier, R.; St-Pierre, S. Can. J. Biochem. Cell Biol. 63, 287-292, 1983
 A;Title: Primary structure determination of *Escherichia coli* heat-stable enterotoxin of *Escherichia coli* serotype O157:H7
 A;Reference number: A30985; MUID:83284515; PMID:6349752
 A;Accession: A30985
 A;Molecule type: protein
 A;Residues: 55-72 <LAZ2>
 A;Experimental source: strain F11
 R;Dallas, W.S. J. Bacteriol. 172, 5490-5493, 1990
 A;Title: The heat-stable toxin I gene from *Escherichia coli* 18D.
 A;Reference number: A36732; MUID:90368614; PMID:2203756
 A;Accession: A36732
 A;Molecule type: DNA
 A;Residues: 1-72 <DAL>
 A;Cross-references: GB:M58746; NID:gl45860; PIDN:AAA62776.1; PID:gl45861
 A;Experimental source: strain 18D
 R;Stieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.; Plasmid 20, 42-53, 1988
 A;Title: Cloning, sequencing, and expression in *Escherichia coli* heat-stable enterotoxin I
 A;Reference number: JT0373; MUID:89202548; PMID:3071819
 A;Accession: JT0374
 A;Molecule type: DNA
 A;Residues: 1-72 <STI>
 R;Sekizaki, T.; Akashi, H.; Terakado, N. Am. J. Vet. Res. 46, 909-912, 1985
 A;Title: Nucleotide sequences of the genes for *Escherichia coli* heat-stable enterotoxin I
 A;Reference number: I51932; MUID:85249571; PMID:2990268
 A;Accession: I51932
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-69, 'P', 71-72 <RES>
 A;Cross-references: GB:M25607; NID:gl47877; PIDN:AAA24653.1; PID:gl47878
 C;Comment: Both heat-stable and heat-labile enterotoxins are produced by pathogenic strains of *Escherichia coli*.
 C;Superfamily: heat-stable enterotoxin ST
 C;Keywords: enterotoxin; heat-stable protein
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-54/Domain: propeptide #status predicted <PRO>
 F;55-72/Product: heat-stable enterotoxin ST-I #status experimental <MAT>
 F;59-64,60-68,63-71/Disulfide bonds: #status predicted

Query Match 57.9%; Score 11; DB 1; Length 72;
 Best Local Similarity 100.0%; Pred. No. 7.2e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YCCELCCNPAC 15
 |||||
 DB 58 YCCELCCNPAC 68

RESULT 5
 S68705
 heat-stable enterotoxin Y-Stc - *Yersinia enterocolitica*
 C;Species: *Yersinia enterocolitica*
 C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
 C;Accession: S68705
 R;Yoshino, K.; Takao, T.; Huang, X.; Murata, H.; Nakao, H.; Takeda, T.; Shimonishi, Y. FEBS Lett. 362, 319-322, 1995
 A;Title: Characterization of a highly toxic, large molecular size heat-stable enterotoxin
 A;Reference number: S68705; MUID:95246844; PMID:7729521
 A;Accession: S68705

A:Molecule type: protein
A:Residues: 1-53 <YOS>
A:Experimental source: strain 86-11
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:41-46,42-50,45-53/Disulfide bonds: #status predicted

Query Match 52.6%; Score 10; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCELCNPAC 15
|||||
Db 41 CCELCNPAC 50

RESULT 6
CHEC2
heat-stable enterotoxin ST-2 - Escherichia coli
C:Species: Escherichia coli
C:Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 09-Jul-2004
C:Accession: A01823
R:Chan, S.K.; Giannella, R.A.
J. Biol. Chem. 256, 7744-7746, 1981
A:Title: Amino acid sequence of heat-stable enterotoxin produced by Escherichia coli pat
A:Reference number: A01823; MUID:81264141; PMID:7021541
A:Accession: A01823
A:Molecule type: protein
A:Residues: 1-18 <CHA>
A:Cross-references: UNIPROT:P01560
A:Experimental source: strain 18D, serotype 0.42:k86:H37
C:Comment: This enterotoxin is one of several, of differing molecular sizes, produced by
idues of the heat-stable enterotoxin ST-1.
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:1-18/Product: heat-stable enterotoxin ST-2 #status experimental <MAT>
F:5-10,6-14,9-17/Disulfide bonds: #status predicted

Query Match 36.8%; Score 7; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YCCELC 11
|||||
Db 4 YCCELC 10

RESULT 7
T19913
hypothetical protein C43F9.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19913
R:Mortimore, B.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19195
A:Accession: T19913
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-248 <WIL>
A:Cross-references: UNIPROT:Q9XUG6; EMBL:282262; PIDN:CAB05152.1; GSPDB:GN000022; CESP:C4
A:Experimental source: clone C43F9
C:Genetics:
A:Gene: CESP:C43F9.5
A:Map position: 4
A:Introns: 47/1; 78/3; 118/1; 199/3

Query Match 36.8%; Score 7; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSNYCCE 8
|||||

Db 181 SSNYCCE 187

RESULT 8

A28953

alpha-conotoxin SI - cone shell (Conus striatus)

C:Species: Conus striatus (striated cone)

C:Date: 30-Jun-1989 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: A28953

R:Zafaralla, G.C.; Ramilo, C.; Gray, W.R.; Karlstrom, R.; Olivera, B.M.; Cruz, L.J.

Biochemistry 27, 7102-7105, 1988

A:Title: Phylogenetic specificity of cholinergic ligands: alpha-conotoxin SI.

A:Reference number: A28953; MUID:89062448; PMID:3196703

A:Accession: A28953

A:Molecule type: protein

A:Residues: 1-13 <ZAF>

A:Cross-references: UNIPROT:P15471

A:Note: This sequence was confirmed by chemical synthesis

C:Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholin

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurot

F:2-7,3-13/Disulfide bonds: #status experimental

F:13/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 31.6%; Score 6; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CCNPAC 15

|||||

Db 2 CCNPAC 7

RESULT 9

NTKXG

alpha-conotoxin GIA [validated] - cone shell (Conus geographus)

N:Alternate names: alpha-Crx-GIA

N:Contains: alpha-conotoxin GI

C:Species: Conus geographus (geography cone)

C:Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 09-Jul-2004

C:Accession: A01782

R:Gray, W.R.; Luque, A.; Olivera, B.M.; Barrett, J.; Cruz, L.J.

J. Biol. Chem. 256, 4734-4740, 1981

A:Title: Peptide toxins from Conus geographus venom.

A:Reference number: A92320; MUID:81191854; PMID:7014556

A:Accession: A01782

A:Molecule type: protein

A:Residues: 1-15 <GRA>

A:Cross-references: UNIPROT:P01519

R:Gray, W.R.; Rivier, J.E.; Galyean, R.; Cruz, L.J.; Olivera, B.M.

J. Biol. Chem. 258, 12247-12251, 1983

A:Title: Conotoxin MI. Disulfide bonding and conformational states.

A:Reference number: A92396; MUID:84032400; PMID:6630187

A:Contents: annotation; disulfide bonds

R:Guddat, L.W.; Shan, L.; Martin, J.L.; Edmundson, A.B.; Gray, W.R.

submitted to the Brookhaven Protein Data Bank, May 1996

A:Reference number: A66253; PDB:1NOT

A:Contents: annotation; X-ray crystallography, 1.2 angstroms, residues 1-13

R:Guddat, L.W.; Martin, J.A.; Shan, L.; Edmundson, A.B.; Gray, W.R.

Biochemistry 35, 11329-11335, 1996

A:Title: Three-dimensional structure of the alpha-conotoxin GI at 1.2 angstroms resoluti

A:Reference number: A58592; MUID:96378624; PMID:8784187

A:Contents: annotation; X-ray crystallography, 1.2 angstroms

R:Pardi, A.; Galdes, A.; Florence, J.; Manicote, D.

Biochemistry 28, 5494-5501, 1989

A:Title: Solution structures of alpha-conotoxin GI determined by two-dimensional NMR spe

A:Reference number: A30629; MUID:89375269; PMID:2775719

A:Contents: annotation; conformation by (1)H-NMR

C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynapt

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; blocked carboxyl en

F:1-15/Product: conotoxin GIA #status experimental <GIA>

F:1-13/Product: conotoxin GI #status experimental <GIC>

F;2-7,3-13/Disulfide bonds: #link GIA #status predicted
 F;2-7,3-13/Disulfide bonds: #link GIC #status experimental
 F;13/Modified site: amidated carboxyl end (Cys) (amide in mature form from following gly
 F;15/Modified site: blocked carboxyl end (Iys) (probably amidated) #status experimental

Query Match 31.6%; Score 6; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCNPAC 15
 |||||
 Db 2 CCNPAC 7

RESULT 10

A54534
 heat-stable enterotoxin - Vibrio mimicus (fragment)
 C;Species: Vibrio mimicus
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-May-1996
 C;Accession: A54534
 R;Arita, M.; Honda, T.; Miwatani, T.; Takeda, T.; Takao, T.; Shimonishi, Y.
 FEMS Microbiol. Lett. 79, 105-110, 1991
 A;Title: Purification and characterization of a heat-stable enterotoxin of Vibrio mimicus
 A;Reference number: A54534
 A;Accession: A54534
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-17 <ARI>
 C;Superfamily: heat-stable enterotoxin ST

Query Match 31.6%; Score 6; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCNPAC 15
 |||||
 Db 7 CCNPAC 12

RESULT 11

A44379
 alpha-conotoxin SII - cone shell (Conus striatus)
 C;Species: Conus striatus (striated cone)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
 C;Accession: A44379
 R;Ramilo, C.A.; Zafaralla, G.C.; Nadaadi, L.; Hammerland, L.G.; Yoshikami, D.; Gray, W.R.
 Biochemistry 31, 9915-9926, 1992
 A;Title: Novel alpha- and omega-conotoxins from Conus striatus venom.
 A;Reference number: A44379; MUID:93003172; PMID:1390774
 A;Accession: A44379
 A;Molecule type: protein
 A;Residues: 1-19 <RAM>
 A;Cross-references: CAS:143294-31-9; PIDN:AAB23762.1; PID:G257934
 A;Experimental source: venom
 A;Note: sequence extracted from NCBI backbone (NCBIP:116000); structure confirmed by che
 C;Comment: This peptide is an acetylcholine receptor blocker.
 C;Superfamily: alpha-conotoxin
 C;Keywords: acetylcholine receptor inhibitor; postsynaptic neurotoxin; venom
 F;2-18,3-8,4-14/Disulfide bonds: #status predicted
 F;19/Modified site: amidated carboxyl end (Ser) #status absent

Query Match 31.6%; Score 6; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCNPAC 15
 |||||
 Db 3 CCNPAC 8

RESULT 12

S34671
 heat-stable enterotoxin - Vibrio cholerae (fragment)

C;Species: Vibrio cholerae
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S34671
 R;Rossolini, G.M.; Lombardi, G.; Guglielmetti, P.

submitted to the EMBL Data Library, July 1993
 A;Description: Detection of the Vibrio cholerae heat-stable enterotoxin gene by polymerase

A;Reference number: S34671
 A;Accession: S34671

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-65 <ROS>

A;Cross-references: UNIPROT:Q56643; EMBL:X74108

C;Superfamily: heat-stable enterotoxin ST

Query Match 31.6%; Score 6; DB 2; Length 65;
 Best Local Similarity 100.0%; Pred. No. 3.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCNPAC 15
 |||||
 Db 59 CCNPAC 64

RESULT 13

S31652
 enterotoxin - Yersinia kristensenii
 C;Species: Yersinia kristensenii
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S31652

R;Ibrahim, A.; Liesack, W.; Stackebrandt, E.
 submitted to the EMBL Data Library, November 1992

A;Reference number: S31652

A;Accession: S31652

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-66 <IBR>

A;Cross-references: UNIPROT:P31518; EMBL:X69218; NID:g48617; PIDN:CAA49152.1; PID:g48618

C;Superfamily: heat-stable enterotoxin ST

Query Match 31.6%; Score 6; DB 2; Length 66;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCNPAC 15
 |||||
 Db 58 CCNPAC 63

RESULT 14

S25659
 heat-stable enterotoxin yst precursor - Yersinia enterocolitica
 C;Species: Yersinia enterocolitica
 C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C;Accession: S25659; A41474; A23114; S65849
 R;Ibrahim, A.; Liesack, W.; Pike, S.; Stackebrandt, E.
 FEMS Microbiol. Lett. 97, 63-66, 1992
 A;Title: The polymerase chain reaction: an epidemiological tool to differentiate between

A;Reference number: S25659

A;Accession: S25659

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-71 <IBR>

A;Cross-references: UNIPROT:P07593; EMBL:X65999; NID:g48611; PIDN:CAA46801.1; PID:g48612

R;Delor, I.; Kaechenbeek, A.; Wauters, G.; Cornelis, G.R.

Infect. Immun. 58, 2983-2988, 1990

A;Title: Nucleotide sequence of yst, the Yersinia enterocolitica gene encoding the heat-

A;Reference number: A41474; MUID:90354067; PMID:2201642

A;Accession: A41474

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-47, 'S', 49-71

A;Cross-references: GH:U09235; NID:g487394; PIDN:AAA18472.1; PID:g487395

R;Takao, T.; Tomimaga, N.; Yoshimura, S.; Shimonishi, Y.; Hara, S.; Inoue, T.; Miyama, A.

Eur. J. Biochem. 152, 199-206, 1985
A:Title: Isolation, primary structure and synthesis of heat-stable enterotoxin produced
A:Reference number: A23114; MUID:86004705; PMID:4043080
A:Accession: A23114
A:Molecule type: protein
A:Residues: 54-71 <TAK>
R:Milulek, A.V.; Delor, I.; Ha Thi, V.; Cornelis, G.R.
Mol. Microbiol. 14, 905-915, 1994
A:Title: Regulation of the Yersinia enterocolitica enterotoxin Yst gene. Influence of g
A:Reference number: S65849; MUID:95231297; PMID:7715452
A:Accession: S65849
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-43 <MIK>
A:Cross-references: EMBL:U09235
C:Genetics:
A:Gene: yst
C:Superfamily: heat-stable enterotoxin ST
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-41/Domain: propeptide #status predicted <PRO>
F:42-71/Product: heat-stable enterotoxin yst #status predicted <MAT>

Query Match 31.6%; Score 6; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 3.8; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Qy 10 CCNPAC 15
Db 63 CCNPAC 68
|||||

RESULT 15

QHVCI
heat-stable enterotoxin ST precursor - Vibrio cholerae
C:Species: Vibrio cholerae
C:Date: 17-Mar-1987 #sequence revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: A1469; A01824; S34464; S34466; S34463
R:Ogawa, A.; Kato, J.I.; Watanabe, H.; Nair, B.G.; Takeda, T.
Infect. Immun. 58, 3325-3329, 1990
A:Title: Cloning and nucleotide sequence of a heat-stable enterotoxin gene from Vibrio c
A:Reference number: A1469; MUID:90382953; PMID:2205577
A:Accession: A1469
A:Molecule type: DNA
A:Residues: 1-78 <OGA>
A:Cross-references: UNIPROT:P04429; GB:M85198; GB:M36061; NID:G155237; PIDN:AAA64889.1;
R:Takao, T.; Shimonishi, Y.; Kobayashi, M.; Nishimura, O.; Arita, M.; Takeda, T.; Honda,
FEBS Lett. 193, 250-254, 1985
A:Title: Amino acid sequence of heat-stable enterotoxin produced by Vibrio cholerae non-
A:Reference number: A01824; MUID:86056320; PMID:4065341
A:Accession: A01824
A:Molecule type: protein
A:Residues: 62-78 <TAK>
A:Experimental source: non-O:1 serovar
R:Yoshino, K.; Miyachi, M.; Takao, T.; Bag, P.K.; Xiaozhe, H.; Nair, G.B.; Takeda, T.; S
FEBS Lett. 326, 83-86, 1993
A:Title: Purification and sequence determination of heat-stable enterotoxin elaborated b
A:Reference number: S34463; MUID:93314823; PMID:8325391
A:Accession: S34464
A:Status: preliminary
A:Molecule type: protein
A:Residues: 61-78 <YO3>
A:Accession: S34466
A:Status: preliminary
A:Molecule type: protein
A:Residues: 51-78 <YOS>
A:Accession: S34465
A:Status: preliminary
A:Molecule type: protein
A:Residues: 60-78 <Y02>
A:Accession: S34463
A:Status: preliminary
A:Molecule type: protein
A:Residues: 62-78 <Y04>

C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-61/Domain: propeptide #status predicted <PRO>
F:62-78/Product: heat-stable enterotoxin ST #status experimental <MAT>
F:64-69,65-73,68-76/Disulfide bonds: #status predicted

Query Match 31.6%; Score 6; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CCNPAC 15
Db 68 CCNPAC 73
|||||

Search completed: March 26, 2005, 17:26:00
Job time : 20.6786 secs

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